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090529

(54) Title: DNA MOLECULES ENCODING MACACA MULATTA ANDROGEN RECEPTOR

(57) Abstract: The present invention discloses the isolation and characterization of cDNA molecules encoding novel androgen receptor (AR) protein from Macaca mulatta. Also within the scope of the disclosure are recombinant vectors, recombinant host cells, methods of screening for modulators of Macaca mulatta AR (rhAR) activity, purified proteins and fusion proteins which comprise all or a portion of the rhAR protein, transgenic mice comprising a transgene encoding the rhAR protein, as well as production of antibodies against AR, or epitopes thereof.

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TITLE OF THE INVENTION

DNA MOLECULES ENCODING MACACA MULATTA ANDROGEN

RECEPTOR

### 5 CROSS-REFERENCE TO RELATED APPLICATIONS

The present application claims priority of U.S. provisional application Serial No. 60/289,573, filed May 8, 2001.

### FIELD OF THE INVENTION

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The present invention relates in part to isolated nucleic acid molecules (polynucleotides) which encode a *Macaca mulatta* (rhesus monkey) androgen receptor (rhAR) protein. The present invention also relates to recombinant vectors and recombinant hosts which contain a DNA fragment encoding rhAR, substantially purified, biologically active forms of rhAR, including precursor and mature forms of the protein, mutant proteins which retain a biological activity of interest, methods associated with identifying compounds which modulate rhAR activity, and non-human animals which have been subject to intervention to effect rhAR activity.

### **BACKGROUND OF THE INVENTION**

The nuclear receptor superfamily, which includes steroid hormone receptors, are small chemical ligand-inducible transcription factors which have been shown to play roles in controlling development, differentiation and physiological function. Isolation of cDNA clones encoding nuclear receptors reveals several characteristics. First, the NH2-terminal regions, or the A/B domain, which vary in length between receptors, are hypervariable with low homology between family members. There are three internal regions of conservation, referred to as domains C, D and E/F. Region C encodes a cysteine-rich region which is referred to as the DNA binding domain (DBD). Regions D and E/F are within the COOH-terminal section of the protein. Region D encodes the hinge domain which is also referred to as the ligand binding domain (LBD). For a review, see Power et al. (1992, Trends in Pharmaceutical Sciences 13: 318-323).

The lipophilic hormones that activate steroid receptors are known to be associated with human diseases. Therefore, the respective nuclear receptors have been identified as possible targets for therapeutic intervention. For a review of the

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mechanism of action of various steroid hormone receptors, see Tsai and O'Malley (1994, Annu. Rev. Biochem. 63: 451-486).

Recent work with non-steroid nuclear receptors has also shown the potential as drug targets for therapeutic intervention. This work reports that peroxisome proliferator activated receptor g (PPARg), identified by a conserved DBD region, promotes adipocyte differentiation upon activation and that thiazolidinediones, a class of antidiabetic drugs, function through PPARg (Tontonoz et al., 1994, *Cell* 79: 1147-1156; Lehmann et al., 1995, *J. Biol. Chem.* 270(22): 12953-12956; Teboul et al., 1995, *J. Biol. Chem.* 270(47): 28183-28187). This indicates that PPARg plays a role in glucose homeostasis and lipid metabolism.

Mangelsdorf et al. (1995, *Cell* 83: 835-839) provide a review of known members of the nuclear receptor superfamily.

U.S. Patent No. 5,614,620, issued to Liao and Chang on March 25, 1997, discloses nucleotide sequences encoding human and rat androgen receptor, along with the complete amino acid sequence within the open reading frame of the respective androgen receptor.

EP 0 365 657 B1 issued to French et al. August 4, 1999, discloses a recombinant DNA molecule encoding a human androgen receptor, along with the amino acid sequences of human androgen receptor protein.

Choong et al. (1998, *J. Mol. Evol.* 47: 334-342) disclose amino acid sequences for non-human primates such as chimpanzee, baboon, lemur and *Macaca fascicularis* (see SEQ ID NO:6 for nucleotide sequence, see also Gen Bank Accession No. U94179 for the nucleotide and amino acid sequence of *Macaca fascicularis* androgen receptor).

Abdelgadir et al. (1999, *Biology of Reproduction* 60:1251-1256) disclose a PCR fragment representing a 5' portion of the *Macaca mulatta* coding region (see also Gen Bank Accession No. AF092930).

It would be advantageous to identify additional genes closely related to the human androgen receptor gene, such as those possessed by nonhuman primates used for pharmacological investigation, which encode an androgen receptor protein. Since the androgen receptor plays an important role in regulating development, reproduction, and maintenance of bone and muscle, such genes, and their expressed functional proteins, will be useful in assays to select for compounds which modulate the biological activity of the androgen receptor, especially as this modulation pertains

to bone formation. The present invention addresses and meets these needs by disclosing isolated nucleic acid molecules which encode a full-length *Macaca mullata* androgen receptor.

### 5 SUMMARY OF THE INVENTION

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The present invention relates in part to isolated nucleic acid molecules (polynucleotides) which encode a full length *Macaca mulatta* androgen receptor (rhAR), and the use of the expressed rhAR or portion thereof in the identification of androgen selective compounds active in bone formation. The isolated polynucleotides of the present invention encode a non-human primate member of this nuclear receptor superfamily. The DNA molecules disclosed herein may be transfected into a host cell of choice wherein the recombinant host cell provides a source for substantial levels of an expressed functional rhAR. Such a functional nuclear receptor will provide for an effective target for use in screening methodology to identify modulators of the androgen receptor, modulators which may be effective in regulating development, reproduction and maintenance of bone and muscle.

A preferred embodiment of the present invention is disclosed in Figure 1A-C and SEQ ID NO: 1, an isolated DNA molecule encoding rhAR. Nucleotide 1051 is polymorphic, present as either a 'A' nucleotide or a 'G' nucleotide (see SEQ ID NO:3).

To this end, another preferred embodiment of the present invention is an isolated DNA molecule as shown in Figure 1A-C and SEQ ID NO:1, except nucleotide 1051 is a 'G' nucleotide instead of a 'A' nucleotide; this isolated DNA molecule being additionally disclosed as SEQ ID NO:3.

The present invention also relates to isolated nucleic acid fragments which encode mRNA expressing a biologically active rhesus monkey androgen receptor which belongs to the nuclear receptor superfamily. A preferred embodiment relates to isolated nucleic acid fragments of SEQ ID NOs:1, and 3 which encode mRNA expressing a biologically functional derivative of rhAR, especially such nucleic acid fragments which encode all or a portion of the LBD and/or DBD regions of the rhAR open reading frame.

The present invention also relates to recombinant vectors and recombinant hosts, both prokaryotic and eukaryotic, transfected and/or transformed to

contain the substantially purified nucleic acid molecules disclosed throughout this specification.

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A preferred aspect of the present invention relates to a substantially purified form of the novel nuclear trans-acting receptor protein, a rhesus androgen receptor protein, which is disclosed in Figures 2 (SEQ ID NO:2) as well as allelic variants of the protein disclosed in SEQ ID NO:2. One allelic variant is disclosed herein as SEQ ID NO:4. The Glu-210 residue of rhAR of SEQ ID NO:2 the parental allele. A single nucleotide change at nucleotide 1051 from 'A' (of SEQ ID NO:1) to 'G' (of SEQ ID NO:3) results in an amino acid change at residue 210 of the rhAR, from the Glu residue of SEQ ID NO:2 to a Gly-210 residue as disclosed in SEQ ID NO:4 as the allelic variant.

Another preferred aspect of the present invention relates to a substantially purified, fully processed (including any proteolytic processing, glycosylation and/or phosphorylation) mature rhAR protein obtained from a recombinant host cell containing a DNA expression vector comprising a nucleotide sequence as set forth in SEQ ID NOs: 1 and 3, or nucleic acid fragments thereof as described above, such DNA expression vectors expressing the respective rhAR protein or rhAR precursor protein. It is especially preferred that the recombinant host cell be a eukaryotic host cell, including but not limited to a mammalian cell line, insect cell line, or yeast.

The present invention also relates to biologically functional derivatives of rhAR as set forth as SEQ ID NOs:2 and 4, including but not limited to rhAR mutants and biologically active fragments such as amino acid substitutions, deletions, additions, amino terminal truncations and carboxy-terminal truncations, such that these fragments provide for proteins or protein fragments of diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists of rhAR function.

The present invention also relates to a non-human transgenic animal which is useful for studying the ability of a variety of compounds to act as modulators of rhAR, or any alternative functional rhAR in vivo by providing cells for culture, in vitro. In reference to the transgenic animals of this invention, reference is made to transgenes and genes. As used herein, a transgene is a genetic construct including a gene. The transgene is integrated into one or more chromosomes in the cells in an animal by methods known in the art. Once integrated, the transgene is carried in at

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least one place in the chromosomes of a transgenic animal. Of course, a gene is a nucleotide sequence that encodes a protein, such as one or a combination of the cDNA clones described herein. The gene and/or transgene may also include genetic regulatory elements and/or structural elements known in the art. A type of target cell for transgene introduction is the embryonic stem cell (ES). ES cells can be obtained from pre-implantation embryos cultured in vitro and fused with embryos (Evans et al., 1981, Nature 292:154-156; Bradley et al., 1984, Nature 309:255-258; Gossler et al., 1986, Proc. Natl. Acad. Sci. USA 83:9065-9069; and Robertson et al., 1986 Nature 322:445-448). Transgenes can be efficiently introduced into the ES cells by a variety of standard techniques such as DNA transfection, microinjection, or by retrovirus-mediated transduction. The resultant transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The introduced ES cells thereafter colonize the embryo and contribute to the germ line of the resulting chimeric animal (Jaenisch, 1988, Science 240: 1468-1474). It will also be within the purview of the skilled artisan to produce transgenic or knock-out invertebrate animals (e.g., C. elegans) which express the rhAR transgene in a wild type background as well in C. elegans mutants knocked out for one or both of the rhAR subunits. These organisms will be helpful in further determining the dominant negative effect of rhAR as well as selecting from compounds which modulate this effect.

The present invention also relates to a non-human transgenic animal which is heterozygous for a functional rhAR gene native to that animal. As used herein, functional is used to describe a gene or protein that, when present in a cell or *in vitro* system, performs normally as if in a native or unaltered condition or environment. The animal of this aspect of the invention is useful for the study of the specific expression or activity of rhAR in an animal having only one functional copy of the gene. The animal is also useful for studying the ability of a variety of compounds to act as modulators of rhAR activity or expression *in vivo* or, by providing cells for culture, *in vitro*. It is reiterated that as used herein, a modulator is a compound that causes a change in the expression or activity of rhAR, or causes a change in the effect of the interaction of rhAR with its ligand(s), or other protein(s). In an embodiment of this aspect, the animal is used in a method for the preparation of a further animal which lacks a functional native AR gene. In another embodiment, the animal of this aspect is used in a method to prepare an animal which expresses the

non-native rhAR gene in the absence of the expression of a native AR gene. In particular embodiments the non-human animal is a mouse.

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In reference to the transgenic animals of this invention, reference is made to transgenes and genes. As used herein, a transgene is a genetic construct including a gene. The transgene is integrated into one or more chromosomes in the cells in an animal by methods known in the art. Once integrated, the transgene is carried in at least one place in the chromosomes of a transgenic animal. Of course, a gene is a nucleotide sequence that encodes a protein, such as rhAR. The gene and/or transgene may also include genetic regulatory elements and/or structural elements known in the art.

An aspect of this invention is a method of producing transgenic animals having a transgene including the non-native rhAR gene on a native AR null background. The method includes providing transgenic animals of this invention whose cells are heterozygous for a native gene encoding a functional rhAR protein and an altered native AR gene. These animals are crossed with transgenic animals of this invention that are hemizygous for a transgene including a non-native rhAR gene to obtain animals that are both heterozygous for an altered native AR gene and hemizygous for a non-native rhAR gene. The latter animals are interbred to obtain animals that are homozygous or hemizygous for the non-native rhAR and are homozygous for the altered native AR gene. In particular embodiments, cell lines are produced from any of the animals produced in the steps of the method.

The transgenic animals of this invention are also useful in studying the tissue and temporal specific expression patterns of a non-native rhAR throughout the animals. The animals are also useful in determining the ability for various forms of wild-type and mutant alleles of a non-native rhAR to rescue the native AR null deficiency. The animals are also useful for identifying and studying the ability of a variety of compounds to act as modulators of the expression or activity of a non-native rhAR in vivo, or by providing cells for culture, for in vitro studies.

Of particular interest are transgenic mice with rhAR where rhAR expression dominates mouse endogenous AR and can be turned on tissue specifically.

As used herein, a "targeted gene" or "Knockout" (KO) is a DNA sequence introduced into the germline of a non-human animal by way of human intervention, including but not limited to, the methods described herein. The targeted genes of the invention include nucleic acid sequences which are designed to

specifically alter cognate endogenous alleles. An altered AR gene should not fully encode the same AR as native to the host animal, and its expression product can be altered to a minor or great degree, or absent altogether. In cases where it is useful to express a non-native rhAR gene in a transgenic animal in the absence of a native AR gene we prefer that the altered AR gene induce a null lethal knockout phenotype in the animal. However a more modestly modified AR gene can also be useful and is within the scope of the present invention.

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A type of target cell for transgene introduction is the embryonic stem cell (ES). ES cells can be obtained from pre-implantation embryos cultured *in vitro* and fused with embryos (Evans et al., 1981, *Nature* 292:154-156; Bradley et al., 1984, *Nature* 309:255-258; Gossler et al., 1986, *Proc. Natl. Acad. Sci.* USA 83:9065-9069; and Robertson et al., 1986 *Nature* 322:445-448). Transgenes can be efficiently introduced into the ES cells by a variety of standard techniques such as DNA transfection, microinjection, or by retrovirus-mediated transduction. The resultant transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The introduced ES cells thereafter colonize the embryo and contribute to the germ line of the resulting chimeric animal (Jaenisch, 1988, *Science* 240: 1468-1474).

The methods for evaluating the targeted recombination events as well as the resulting knockout mice are readily available and known in the art. Such methods include, but are not limited to DNA (Southern) hybridization to detect the targeted allele, polymerase chain reaction (PCR), polyacrylamide gel electrophoresis (PAGE) and Western blots to detect DNA, RNA and protein.

The present invention also relates to polyclonal and monoclonal antibodies raised in response to rhAR, or a biologically functional derivative thereof. In particular, antibodies to the A/B domain and the hinge domain, (D domain) are preferred. To this end, the DNA molecules, RNA molecules, recombinant protein and antibodies of the present invention may be used to screen and measure levels of rhAR. The recombinant proteins, DNA molecules, RNA molecules and antibodies lend themselves to the formulation of kits suitable for the detection and typing of rhAR.

The present invention also relates assays utilized to identify compounds that modulate rhAR activity. One aspect of this portion of the invention is shown in Example Section 2, an in vitro binding assay using a GST-rhARLBD fusion protein. Other assays are contemplated, including but not limited to using

rhAR cDNA clones and/or expressed proteins in co-transfection assays to measure bioactivity of compounds, as well as mammalian two-hybrid assays to test the effect of compounds on NH<sub>2</sub>- and COOH-terminus interaction of *Macaca mulatta* AR. Such assays are described *infra*.

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It is an object of the present invention to provide an isolated nucleic acid molecule which encodes a novel form of a nuclear receptor protein such as human rhAR, human nuclear receptor protein fragments of full length proteins such as rhAR, and mutants which are derivatives of SEQ ID NOs:2 and 4. Any such polynucleotide includes but is not necessarily limited to nucleotide substitutions, deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists for rhAR function.

Another object of this invention is tissue typing using probes or antibodies of this invention. In a particular embodiment, polynucleotide probes are used to identify tissues expressing rhAR mRNA. In another embodiment, probes or antibodies can be used to identify a type of tissue based on rhAR expression or display of rhAR receptors.

It is a further object of the present invention to provide rhAR proteins or protein fragments encoded by the nucleic acid molecules referred to in the preceding paragraphs, including such rhAR proteins which are expressed within host cells transfected with a DNA expression vector which contains an rhAR nucleotide sequence as disclosed herein.

It is a further object of the present invention to provide recombinant vectors and recombinant host cells which comprise a nucleic acid sequence encoding rhAR or a biological equivalent thereof.

It is an object of the present invention to provide a substantially purified form of rhAR, as set forth in SEQ ID NOs:2 and 4.

It is an object of the present invention to provide for biologically functional derivatives of rhAR, including but not necessarily limited to amino acid substitutions, deletions, additions, amino terminal truncations and carboxy-terminal truncations such that these fragment and/or mutants provide for proteins or protein fragments of diagnostic, therapeutic or prophylactic use.

It is also an object of the present invention to provide for rhAR-based in-frame fusion constructions, methods of expressing these fusion constructions and biological equivalents disclosed herein, related assays, recombinant cells expressing these constructs, the expressed fusion proteins, and agonistic and/or antagonistic compounds identified through the use of DNA molecules encoding these rhAR-based fusion proteins. A preferred fusion construct is one which encodes all or a portion of the LBD and/or DBD regions of the rhAR open reading frame. A preferred fusion protein is one which is expressed from such a construct.

It is also an object of the present invention to provide for assays to identify compounds which modulate rhAR activity.

As used herein, "AR" refers to -- androgen receptor --.
As used herein, "rhAR" refers to -- Macaca mulatta androgen receptor

As used herein, "DBD" refers to -- DNA binding domain --.
As used herein, "LBD" refers to -- ligand binding domain --.
As used herein, "SARM" refers to -- selective androgen receptor

As used herein, the term "mammalian host" refers to any mammal, including a human being.

As used herein, "R1881" refers to methyltrieneolone, also known as 17b-hydroxy-17-methylestra-4,9,11-trien-3-one, the preparation of which is described in Vellux et al., 1963, *Compt. Rend.* 257: 569 et seq.

### BRIEF DESCRIPTION OF THE DRAWINGS

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modulator --.

Figure 1A-C shows the nucleotide sequence (SEQ ID NO: 1) which comprises the open reading frame encoding the rhAR. Underlined nucleotide 1051 ('A') is the site of an allelic variant, which may also be represented by a'G' residue (as disclosed in SEQ ID NO:3).

Figure 2 shows the amino acid sequence (SEQ ID NO: 2) of rhAR. The region in bold and underlined (from residue 535 to residue 600 of SEQ ID NO:2) is the DNA binding domain (DBD). Residue 210 (Glu residue also in bold and underlined) is the site of an allelic variant which may also be represented by a Gly residue (as encoded by SEQ ID NO:3 and disclosed herein as SEQ ID NO:4).

Figure 3A-F shows the coding (SEQ ID NO:1) and anticoding (SEQ ID NO:5) strands which comprises the open reading frame for the rhesus androgen receptor protein (SEQ ID NO:2). The underlined portion (i.e., from amino acid residue 535 to amino acid residue 600 of SEQ ID NO:2) represents the DBD region of expressed rhAR protein.

### DETAILED DESCRIPTION OF THE INVENTION

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The present invention relates to the identification and cloning of genes encoding full length *Macaca mulatta* androgen receptor (rhAR) and their use in the identification of tissue selective androgen compounds, including those active in bone formation, myoanabolism, treatment of sarcopenia, relief of post-menopausal symptoms, treatment of benign prostatic hyperplasia, treatment of acne, treatment of hirsutism, treatment of male hypogonadism, prevention and treatment of prostate cancer, management of lipids, treatment of atherosclerosis, prevention and treatment of breast cancer. The androgen receptor is a member of the nuclear receptor superfamily. The superfamily is composed of a group of structurally related receptors but regulated by chemically distinct ligands. The common structure for them is a conserved DNA binding domain (DBD) located in the center of the peptide and a conserved ligand-binding domain (LBD) at the C-terminus. Eight out of the nine non-variant cysteines form two type II zinc fingers which distinguish them from other DNA-binding proteins.

The present invention relates to isolated nucleic acid molecules (polynucleotides) which encode novel *Macaca mulatta* (rhesus monkey) androgen receptor (rhAR). The isolated polynucleotides of the present invention encode a non-primate member of this nuclear receptor superfamily. The DNA molecules disclosed herein may be transfected into a host cell of choice wherein the recombinant host cell provides a source for substantial levels of an expressed, substantially purified, functional recombinant rhAR, which also forms a portion of the present invention. As noted herein, such a functional nuclear receptor will provide for an effective target for use in screening methodology to identify modulators of the androgen receptor, modulators which may be effective in regulating development, reproduction and maintenance of bone and muscle, treatment of prostate disease, regulation of lipid metabolism and hippocampal function. It is also known that abnormal function of AR can cause prostate cancer. Accumulated

information has also indicated that androgen deficiency results in various abnormalities of bone metabolism, such as increased bone loss. Androgen therapy has been used widely to treat a variety of disorders in both men and women. However, the development of an androgen modulator with desirable effect (i.e., bone promotion) and less side effect (i.e., aggressive behavior, acne) has not been achieved. Recent progress in hormone replacement therapy has proven the possibility in developing selective androgen receptor modulators (SARMs). J. of Clinical Endocrinology & Metabolism, 84(10): 3459 (1999). Therefore, a compound screening system using AR, such as the rhAR disclosed herein, is needed for safe androgen drug development.

A preferred embodiment of the present invention is disclosed in Figure 1A-C and SEQ ID NO: 1, an isolated DNA molecule encoding rhAR. Nucleotide 1051 is polymorphic, present as either a 'A' nucleotide or a 'G' nucleotide (see SEQ ID NO:3). This embodiment is shown as follows, with 1051-A being bolded and underlined:

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1 CCCAAAAAT AAAAACAAAC AAAAACAAAA CAAAACAAAA AAAACGAATA AAGAAAAGG TAATAACTCA GTTCTTATTT GCACCTACTT CCAGTGGACA 101 CTGAATTTGG AAGGTGGAGG ATTCTTGTTT TTTCTTTTAA GATCGGGCAT 151 CTTTTGAATC TACCCCTCAA GTGTTAAGAG ACAGACTGTG AGCCTAGCAG 20 GGCAGATCTT GTCCACCGTG TGTCTTCTTT TGCAGGAGAC TTTGAGGCTG 201 TCAGAGCGCT TTTTGCGTGG TTGCTCCCGC AAGTTTCCTT CTCTGGAGCT 251 301 TCCCGCAGGT GGGCAGCTAG CTGCAGCGAC TACCGCATCA TCACAGCCTG TTGAACTCTT CTGAGCAAGA GAAGGGGAGG CGGGGTAAGG GAAGTAGGTG 351 401 GAAGATTCAG CCAAGCTCAA GGATGGAGGT GCAGTTAGGG CTGGGGAGGG 25 TCTACCCTCG GCCGCCGTCC AAGACCTACC GAGGAGCTTT CCAGAATCTG 451 501 TTCCAGAGCG TGCGCGAAGT GATCCAGAAC CCGGGCCCCA GGCACCCAGA GGCCGCGAGC GCAGCACCTC CCGGCGCCAG TTTGCAGCAG CAGCAGCAGC 551 AGCAGCAAGA AACTAGCCCC CGGCAACAGC AGCAGCAGCA GCAGGGTGAG 601 GATGGTTCTC CCCAAGCCCA TCGTAGAGGC CCCACAGGCT ACCTGGTCCT 651 30 701 GGATGAGGAA CAGCAGCCTT CACAGCCTCA GTCAGCCCCG GAGTGCCACC 751 CCGAGAGAGG TTGCGTCCCA GAGCCTGGAG CCGCCGTGGC CGCCGGCAAG GGGCTGCCGC AGCAGCTGCC AGCACCTCCG GACGAGGATG ACTCAGCTGC 801 CCCATCCACG TTGTCTCTGC TGGGCCCCAC TTTCCCCGGC TTAAGCAGCT 851 GCTCCGCCGA CCTTAAAGAC ATCCTGAGCG AGGCCAGCAC CATGCAACTC 901

|    | 951  | CTTCAGCAAC                         | AGCAGCAGGA         | AGCAGTATCC         | GAAGGCAGCA | GCAGCGGGAG |
|----|------|------------------------------------|--------------------|--------------------|------------|------------|
|    | 1001 | AGCGAGGGAG                         | GCCTCGGGGG         | CTCCCACTTC         | CTCCAAGGAC | AATTACTTAG |
|    | 1051 | $\underline{\mathbf{A}}$ GGGCACTTC | GACCATTTCT         | GACAGCGCCA         | AGGAGCTGTG | TAAGGCAGTG |
|    | 1101 | TCGGTGTCCA                         | TGGGCTTGGG         | TGTGGAGGCG         | TTGGAGCATC | TGAGTCCAGG |
| 5  | 1151 | GGAACAGCTT                         | CGGGGGGATT         | GCATGTACGC         | CCCAGTTTTG | GGAGTTCCAC |
|    | 1201 | CCGCTGTGCG                         | TCCCACTCCG         | TGTGCCCCAT         | TGGCCGAATG | CAAAGGTTCT |
|    | 1251 | CTGCTAGACG                         | ACAGCGCAGG         | CAAGAGCACT         | GAAGATACTG | CTGAGTATTC |
|    | 1301 | CCCTTTCAAG                         | GGAGGTTACA         | CCAAAGGGCT         | AGAAGGCGAG | AGCCTAGGCT |
|    | 1351 | GCTCTGGCAG                         | CGCTGCAGCA         | GGGAGCTCCG         | GGACACTTGA | ACTGCCGTCC |
| 10 | 1401 | ACCCTGTCTC                         | TCTACAAGTC         | CGGAGCACTG         | GACGAGGCAG | CTGCGTACCA |
|    | 1451 | GAGTCGCGAC                         | TACTACAACT         | TTCCACTGGC         | TCTGGCCGGG | CCGCCGCCCC |
|    | 1501 | CTCCACCGCC                         | TCCCCATCCC         | CACGCTCGCA         | TCAAGCTGGA | GAACCCGCTG |
|    | 1551 | GACTATGGCA                         | GCGCCTGGGC         | GGCTGCGGCG         | GCGCAGTGCC | GCTATGGGGA |
|    | 1601 | CCTGGCGAGC                         | ${\tt CTGCATGGCG}$ | CGGGTGCAGC         | GGGACCCGGC | TCTGGGTCAC |
| 15 | 1651 | CCTCAGCGGC                         | CGCTTCCTCA         | TCCTGGCACA         | CTCTCTTCAC | AGCCGAAGAA |
|    | 1701 | $\tt GGCCAGTTGT$                   | ATGGACCGTG         | TGGTGGTGGG         | GGCGGCGGCG | GTGGCGGCGG |
|    | 1751 | CGGCGGCGGC                         | GCAGGCGAGG         | CGGGAGCTGT         | AGCCCCCTAC | GGCTACACTC |
|    | 1801 | GGCCACCTCA                         | GGGGCTGGCG         | GGCCAGGAAG         | GCGACTTCAC | CGCACCTGAT |
|    | 1851 | GTGTGGTACC                         | ${\tt CTGGCGGCAT}$ | GGTGAGCAGA         | GTGCCCTATC | CCAGTCCCAC |
| 20 | 1901 | ${\tt TTGTGTCAAA}$                 | ${\tt AGCGAGATGG}$ | GCCCTGGAT          | GGATAGCTAC | TCCGGACCTT |
|    | 1951 | ACGGGGACAT                         | $\tt GCGTTTGGAG$   | ACTGCCAGGG         | ACCATGTTTT | GCCAATTGAC |
|    | 2001 | TATTACTTTC                         | CACCCCAGAA         | GACCTGCCTG         | ATCTGTGGAG | ATGAAGCTTC |
|    | 2051 | ${\tt TGGGTGTCAC}$                 | ${\tt TATGGAGCTC}$ | ${\tt TCACATGTGG}$ | AAGCTGCAAG | GTCTTCTTCA |
|    | 2101 | AAAGAGCCGC                         | TGAAGGGAAA         | CAGAAGTACC         | TGTGTGCCAG | CAGAAATGAT |
| 25 | 2151 | TGCACTATTG                         | ATAAATTCCG         | AAGGAAAAAT         | TGTCCATCTT | GCCGTCTTCG |
|    | 2201 | GAAATGTTAT                         | GAAGCAGGGA         | ${\tt TGACTCTGGG}$ | AGCCCGGAAG | CTGAAGAAAC |
|    | 2251 | TTGGTAATCT                         | GAAACTACAG         | GAGGAAGGAG         | AGGCTTCCAG | CACCACCAGC |
|    | 2301 | CCCACTGAGG                         | AGACAGCCCA         | GAAGCTGACA         | GTGTCACACA | TTGAAGGCTA |
|    | 2351 | TGAATGTCAG                         | CCCATCTTTC         | TGAATGTCCT         | GGAGGCCATT | GAGCCAGGTG |
| 30 | 2401 | ${\tt TGGTGTGTGC}$                 | TGGACATGAC         | AACAACCAGC         | CCGACTCCTT | CGCAGCCTTG |
|    | 2451 | CTCTCTAGCC                         | TCAATGAACT         | GGGAGAGAGA         | CAGCTTGTAC | ATGTGGTCAA |
|    | 2501 | GTGGGCCAAG                         | GCCTTGCCTG         | GCTTCCGCAA         | CTTACACGTG | GACGACCAGA |
|    | 2551 | TGGCTGTCAT                         | TCAGTACTCC         | TGGATGGGGC         | TCATGGTGTT | TGCCATGGGC |
|    | 2601 | TGGCGATCCT                         | TCACCAATGT         | CAACTCCAGG         | ATGCTCTACT | TTGCCCCTGA |

2651 TCTGGTTTTC AATGAGTACC GCATGCACAA ATCCCGGATG TACAGCCAGT GTGTCCGAAT GAGGCACCTC TCTCAAGAGT TTGGATGGCT CCAAATCACC 2701 CCCCAGGAAT TCCTGTGCAT GAAAGCGCTG CTACTCTTCA GCATTATTCC 2751 AGTGGATGGG CTGAAAAATC AAAAATTCTT TGATGAACTT CGAATGAACT 2801 5 2851 ACATCAAGGA ACTCGATCGT ATCATTGCAT GCAAAAGAAA AAATCCCACA 2901 TCCTGCTCAA GGCGTTTCTA CCAGCTCACC AAGCTCCTGG ACTCCGTGCA GCCTATTGCG AGAGAGCTGC ATCAGTTCAC TTTTGACCTG CTAATCAAGT 2951 CACACATGGT GAGCGTGGAC TTTCCGGAAA TGATGGCAGA GATCATCTCT 3001 3051 GTGCAAGTGC CCAAGATCCT TTCTGGGAAA GTCAAGCCCA TCTATTTCCA 10 3101 CACCCAGTGA AGCATTGGAA ATCCCTATTT CCTCACCCCA GCTCATGCCC CCTTTCAGAT GTCTTCTGCC TGTTA (SEQ ID NO:1).

As noted above, nucleotide 1051 represents a single nucleotide polymorphism (SNP). To this end, another preferred embodiment of the present invention is an isolated DNA molecule as shown in Figure 1A-C and SEQ ID NO:1, except nucleotide 1051 is a 'G' nucleotide instead of a 'A' nucleotide, this isolated DNA molecule being additionally disclosed as SEQ ID NO:3, as follows, with 1051-G being bolded and underlined:

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CCCAAAAAT AAAAACAAAC AAAAACAAAA CAAAACAAAA AAAACGAATA 51 AAGAAAAGG TAATAACTCA GTTCTTATTT GCACCTACTT CCAGTGGACA 20 101 CTGAATTTGG AAGGTGGAGG ATTCTTGTTT TTTCTTTTAA GATCGGGCAT 151 CTTTTGAATC TACCCCTCAA GTGTTAAGAG ACAGACTGTG AGCCTAGCAG 201 GGCAGATCTT GTCCACCGTG TGTCTTCTTT TGCAGGAGAC TTTGAGGCTG 251 TCAGAGCGCT TTTTGCGTGG TTGCTCCCGC AAGTTTCCTT CTCTGGAGCT 301 TCCCGCAGGT GGGCAGCTAG CTGCAGCGAC TACCGCATCA TCACAGCCTG 25 351 TTGAACTCTT CTGAGCAAGA GAAGGGGAGG CGGGGTAAGG GAAGTAGGTG 401 GAAGATTCAG CCAAGCTCAA GGATGGAGGT GCAGTTAGGG CTGGGGAGGG 451 TCTACCCTCG GCCGCCGTCC AAGACCTACC GAGGAGCTTT CCAGAATCTG 501 TTCCAGAGCG TGCGCGAAGT GATCCAGAAC CCGGGCCCCA GGCACCCAGA GGCCGCGAGC GCAGCACCTC CCGGCGCCAG TTTGCAGCAG CAGCAGCAGC 551 30 AGCAGCAAGA AACTAGCCCC CGGCAACAGC AGCAGCAGCA GCAGGGTGAG 601 651 GATGGTTCTC CCCAAGCCCA TCGTAGAGGC CCCACAGGCT ACCTGGTCCT 701 GGATGAGGAA CAGCAGCCTT CACAGCCTCA GTCAGCCCCG GAGTGCCACC 751 CCGAGAGAGG TTGCGTCCCA GAGCCTGGAG CCGCCGTGGC CGCCGGCAAG 801 GGGCTGCCGC AGCAGCTGCC AGCACCTCCG GACGAGGATG ACTCAGCTGC

|    | 851  | CCCATCCACG         | TTGTCTCTGC         | TGGGCCCCAC | TTTCCCCGGC         | TTAAGCAGCT |
|----|------|--------------------|--------------------|------------|--------------------|------------|
|    | 901  | GCTCCGCCGA         | CCTTAAAGAC         | ATCCTGAGCG | AGGCCAGCAC         | CATGCAACTC |
|    | 951  | CTTCAGCAAC         | AGCAGCAGGA         | AGCAGTATCC | GAAGGCAGCA         | GCAGCGGGAG |
|    | 1001 | AGCGAGGGAG         | GCCTCGGGGG         | CTCCCACTTC | CTCCAAGGAC         | AATTACTTAG |
| 5  | 1051 | <b>G</b> GGGCACTTC | GACCATTTCT         | GACAGCGCCA | AGGAGCTGTG         | TAAGGCAGTG |
|    | 1101 | TCGGTGTCCA         | TGGGCTTGGG         | TGTGGAGGCG | TTGGAGCATC         | TGAGTCCAGG |
|    | 1151 | GGAACAGCTT         | CGGGGGGATT         | GCATGTACGC | CCCAGTTTTG         | GGAGTTCCAC |
|    | 1201 | CCGCTGTGCG         | TCCCACTCCG         | TGTGCCCCAT | ${\tt TGGCCGAATG}$ | CAAAGGTTCT |
|    | 1251 | CTGCTAGACG         | ACAGCGCAGG         | CAAGAGCACT | GAAGATACTG         | CTGAGTATTC |
| 10 | 1301 | CCCTTTCAAG         | GGAGGTTACA         | CCAAAGGGCT | AGAAGGCGAG         | AGCCTAGGCT |
|    | 1351 | GCTCTGGCAG         | CGCTGCAGCA         | GGGAGCTCCG | GGACACTTGA         | ACTGCCGTCC |
|    | 1401 | ACCCTGTCTC         | ${\tt TCTACAAGTC}$ | CGGAGCACTG | GACGAGGCAG         | CTGCGTACCA |
|    | 1451 | GAGTCGCGAC         | TACTACAACT         | TTCCACTGGC | TCTGGCCGGG         | CCGCCGCCCC |
|    | 1501 | CTCCACCGCC         | TCCCCATCCC         | CACGCTCGCA | TCAAGCTGGA         | GAACCCGCTG |
| 15 | 1551 | GACTATGGCA         | GCGCCTGGGC         | GGCTGCGGCG | GCGCAGTGCC         | GCTATGGGGA |
|    | 1601 | CCTGGCGAGC         | CTGCATGGCG         | CGGGTGCAGC | GGGACCCGGC         | TCTGGGTCAC |
|    | 1651 | CCTCAGCGGC         | CGCTTCCTCA         | TCCTGGCACA | CTCTCTTCAC         | AGCCGAAGAA |
|    | 1701 | GGCCAGTTGT         | ATGGACCGTG         | TGGTGGTGGG | GGCGGCGCG          | GTGGCGGCGG |
|    | 1751 | CGGCGGCGGC         | GCAGGCGAGG         | CGGGAGCTGT | AGCCCCCTAC         | GGCTACACTC |
| 20 | 1801 | GGCCACCTCA         | GGGGCTGGCG         | GGCCAGGAAG | GCGACTTCAC         | CGCACCTGAT |
|    | 1851 | GTGTGGTACC         | CTGGCGGCAT         | GGTGAGCAGA | GTGCCCTATC         | CCAGTCCCAC |
|    | 1901 | TTGTGTCAAA         | AGCGAGATGG         | GCCCTGGAT  | GGATAGCTAC         | TCCGGACCTT |
|    | 1951 | ACGGGGACAT         | GCGTTTGGAG         | ACTGCCAGGG | ACCATGTTTT         | GCCAATTGAC |
|    | 2001 | TATTACTTTC         | CACCCCAGAA         | GACCTGCCTG | ATCTGTGGAG         | ATGAAGCTTC |
| 25 | 2051 | TGGGTGTCAC         | TATGGAGCTC         | TCACATGTGG | AAGCTGCAAG         | GTCTTCTTCA |
|    | 2101 | AAAGAGCCGC         | TGAAGGGAAA         | CAGAAGTACC | TGTGTGCCAG         | CAGAAATGAT |
|    | 2151 | TGCACTATTG         | ATAAATTCCG         | AAGGAAAAAT | TGTCCATCTT         | GCCGTCTTCG |
|    | 2201 | GAAATGTTAT         | GAAGCAGGGA         | TGACTCTGGG | AGCCCGGAAG         | CTGAAGAAAC |
|    | 2251 | TTGGTAATCT         | GAAACTACAG         | GAGGAAGGAG | AGGCTTCCAG         | CACCACCAGC |
| 30 | 2301 | CCCACTGAGG         | AGACAGCCCA         | GAAGCTGACA | GTGTCACACA         | TTGAAGGCTA |
|    | 2351 | TGAATGTCAG         | CCCATCTTTC         | TGAATGTCCT | GGAGGCCATT         | GAGCCAGGTG |
|    | 2401 | TGGTGTGTGC         | TGGACATGAC         | AACAACCAGC | CCGACTCCTT         | CGCAGCCTTG |
|    | 2451 | CTCTCTAGCC         | TCAATGAACT         | GGGAGAGAGA | CAGCTTGTAC         | ATGTGGTCAA |
|    | 2501 | GTGGGCCAAG         | GCCTTGCCTG         | GCTTCCGCAA | CTTACACGTG         | GACGACCAGA |

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2551
          TGGCTGTCAT TCAGTACTCC TGGATGGGGC TCATGGTGTT TGCCATGGGC
          TGGCGATCCT TCACCAATGT CAACTCCAGG ATGCTCTACT TTGCCCCTGA
    2601
          TCTGGTTTTC AATGAGTACC GCATGCACAA ATCCCGGATG TACAGCCAGT
    2651
          GTGTCCGAAT GAGGCACCTC TCTCAAGAGT TTGGATGGCT CCAAATCACC
    2701
          CCCCAGGAAT TCCTGTGCAT GAAAGCGCTG CTACTCTTCA GCATTATTCC
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    2751
    2801
          AGTGGATGGG CTGAAAAATC AAAAATTCTT TGATGAACTT CGAATGAACT
          ACATCAAGGA ACTCGATCGT ATCATTGCAT GCAAAAGAAA AAATCCCACA
    2851
          TCCTGCTCAA GGCGTTTCTA CCAGCTCACC AAGCTCCTGG ACTCCGTGCA
    2901
          GCCTATTGCG AGAGAGCTGC ATCAGTTCAC TTTTGACCTG CTAATCAAGT
    2951
10
    3001
          CACACATGGT GAGCGTGGAC TTTCCGGAAA TGATGGCAGA GATCATCTCT
          GTGCAAGTGC CCAAGATCCT TTCTGGGAAA GTCAAGCCCA TCTATTTCCA
    3051
          CACCCAGTGA AGCATTGGAA ATCCCTATTT CCTCACCCCA GCTCATGCCC
    3101
    3151
          CCTTTCAGAT GTCTTCTGCC TGTTA (SEQ ID NO:3).
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The above-exemplified isolated DNA molecules, comprise the

15 following characteristics:

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(SEQ ID NO:1) - 3175 nuc.:initiating Met (nuc. 423-425) and "TCA" term. codon (nuc.3106-3108), with a polymorphic site at nucleotide 1051 ('A'), the open reading frame resulting in an expressed protein of 895 amino acids, as set forth in SEQ ID NO:2, with amino acid residue 210 being a Glu (E) residue.

(SEQ ID NO:3) - 3175 nuc.:initiating Met (nuc. 423-425) and "TCA" term. codon (nuc.3106-3108), with a polymorphic site at nucleotide 1051 ('G'), the open reading frame resulting in an expressed protein of 895 amino acids, as set forth in SEQ ID NO:4, with amino acid residue 210 being a Gly (G) residue.

The present invention also relates to isolated nucleic acid fragments which encode mRNA expressing a biologically active rhesus monkey androgen receptor which belongs to the nuclear receptor superfamily. A preferred embodiment relates to isolated nucleic acid fragments of SEQ ID NOs:1 and 3 which encode mRNA expressing a biologically functional derivative of rhAR. Any such nucleic acid fragment will encode either a protein or protein fragment comprising at least an intracellular DNA-binding domain and/or ligand binding domain, domains conserved throughout the rhAR nuclear receptor family domain which exist in rhAR (SEQ ID NOs: 2 and 4). Any such polynucleotide includes but is not necessarily limited to nucleotide substitutions (including but not limited to SNPs, such as single nucleotide substitutions as disclosed herein, as well as deletion and/or insertions which fall

within the known working definition of a SNP), deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists of rhAR.

The isolated nucleic acid molecule of the present invention may include a deoxyribonucleic acid molecule (DNA), such as genomic DNA and complementary DNA (cDNA), which may be single (coding or noncoding strand) or double stranded, as well as synthetic DNA, such as a synthesized, single stranded polynucleotide. The isolated nucleic acid molecule of the present invention may also include a ribonucleic acid molecule (RNA). The preferred template is DNA.

It is known that there is a substantial amount of redundancy in the various codons which code for specific amino acids. Therefore, this invention is also directed to those DNA sequences encode RNA comprising alternative codons that

code for the eventual translation of the identical amino acid, as shown below:

A=Ala=Alanine: codons GCA, GCC, GCG, GCU

C=Cys=Cysteine: codons UGC, UGU

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D=Asp=Aspartic acid: codons GAC, GAU

E=Glu=Glutamic acid: codons GAA, GAG

20 F=Phe=Phenylalanine: codons UUC, UUU

G=Gly=Glycine: codons GGA, GGC, GGG, GGU

H=His =Histidine: codons CAC, CAU

I=Ile =Isoleucine: codons AUA, AUC, AUU

K=Lys=Lysine: codons AAA, AAG

25 L=Leu=Leucine: codons UUA, UUG, CUA, CUC, CUG, CUU

M=Met=Methionine: codon AUG

N=Asp=Asparagine: codons AAC, AAU

P=Pro=Proline: codons CCA, CCC, CCG, CCU

Q=Gln=Glutamine: codons CAA, CAG

30 R=Arg=Arginine: codons AGA, AGG, CGA, CGC, CGG, CGU

S=Ser=Serine: codons AGC, AGU, UCA, UCC, UCG, UCU

T=Thr=Threonine: codons ACA, ACC, ACG, ACU

V=Val=Valine: codons GUA, GUC, GUG, GUU

W=Trp=Tryptophan: codon UGG

Y=Tyr=Tyrosine: codons UAC, UAU.

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Therefore, the present invention discloses codon redundancy that may result in differing DNA molecules expressing an identical protein. For purposes of this specification, a sequence bearing one or more replaced codons will be defined as a degenerate variation. Also included within the scope of this invention are mutations either in the DNA sequence or the translated protein, which do not substantially alter the ultimate physical properties of the expressed protein. For example, substitution of valine for leucine, arginine for lysine, or asparagine for glutamine may not cause a change in functionality of the polypeptide.

It is known that DNA sequences coding for a peptide may be altered so as to code for a peptide having properties that are different than those of the naturally occurring peptide. Methods of altering the DNA sequences include but are not limited to site directed mutagenesis. Examples of altered properties include but are not limited to changes in the affinity of an enzyme for a substrate or a receptor for a ligand.

As used herein, "purified" and "isolated" may be utilized interchangeably to stand for the proposition that the nucleic acid, protein, or respective fragment thereof in question has been substantially removed from its *in vivo* environment so that it may be manipulated by the skilled artisan, such as but not limited to nucleotide sequencing, restriction digestion, site-directed mutagenesis, and subcloning into expression vectors for a nucleic acid fragment as well as obtaining the protein or protein fragment in pure quantities so as to afford the opportunity to generate polyclonal antibodies, monoclonal antibodies, amino acid sequencing, and peptide digestion. Therefore, the nucleic acids claimed herein may be present in whole cells or in cell lysates or in a partially purified or substantially purified form. A nucleic acid is considered substantially purified when it is purified away from environmental contaminants. Thus, a nucleic acid sequence isolated from cells is considered to be substantially purified when purified from cellular components by standard methods while a chemically synthesized nucleic acid sequence is considered to be substantially purified when purified from its chemical precursors.

Any of a variety of procedures may be used to clone rhAR. These methods include, but are not limited to, (1) a RACE PCR cloning technique (Frohman, et al., 1988, *Proc. Natl. Acad. Sci. USA* 85: 8998-9002). 5' and/or 3' RACE may be performed to generate a full length cDNA sequence. This strategy

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involves using gene-specific oligonucleotide primers for PCR amplification of rhAR cDNA. These gene-specific primers are designed through identification of an expressed sequence tag (EST) nucleotide sequence which has been identified by searching any number of publicly available nucleic acid and protein databases; (2) direct functional expression of the rhAR following the construction of a rhARcontaining cDNA library in an appropriate expression vector system; (3) screening a rhAR-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a labeled degenerate oligonucleotide probe designed from the amino acid sequence of the rhAR protein; (4) screening a rhAR-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a partial cDNA encoding the rhAR protein. This partial cDNA is obtained by the specific PCR amplification of rhAR DNA fragments through the design of degenerate oligonucleotide primers from the amino acid sequence known for other nuclear receptors which are related to the rhAR protein; (5) screening a rhAR-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a partial cDNA encoding the rhAR protein. This strategy may also involve using genespecific oligonucleotide primers for PCR amplification of rhAR cDNA identified as an EST as described above; or (6) designing 5' and 3' gene specific oligonucleotides using SEQ ID NO:1 or 3 as a template so that either the full-length cDNA may be generated by known PCR techniques, or a portion of the coding region may be generated by these same known PCR techniques to generate and isolate a portion of the coding region to use as a probe to screen one of numerous types of cDNA and/or genomic libraries in order to isolate a full-length version of the nucleotide molecule encoding rhAR.

It is readily apparent to those ordinarily skilled in the art that other types of libraries, as well as libraries constructed from other cell types-or species types, may be useful for isolating a rhAR-encoding DNA or a rhAR homologue. Other types of libraries include, but are not limited to, cDNA libraries derived from other cells or cell lines other than rhAR cells or tissue such as murine cells, rodent cells or any other such vertebrate host which may contain rhAR-encoding DNA. Additionally a rhAR gene and homologues may be isolated by oligonucleotide- or polynucleotide-based hybridization screening of a vertebrate genomic library, including but not limited to, a murine genomic library, a rodent genomic library, as well as concomitant rhAR genomic DNA libraries.

It is readily apparent to those skilled in the art that suitable cDNA libraries may be prepared from cells or cell lines which have rhAR activity. The selection of cells or cell lines for use in preparing a cDNA library to isolate a cDNA encoding rhAR may be done by first measuring cell-associated rhAR activity using any known assay available for such a purpose.

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Preparation of cDNA libraries can be performed by standard techniques well known in the art. Well known cDNA library construction techniques can be found for example, in Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory, Cold Spring Harbor, New York. Complementary DNA libraries may also be obtained from numerous commercial sources, including but not limited to Clontech Laboratories, Inc. and Stratagene.

It is also readily apparent to those skilled in the art that DNA encoding rhAR may also be isolated from a suitable genomic DNA library. Construction of genomic DNA libraries can be performed by standard techniques well known in the art. Well known genomic DNA library construction techniques can be found in Sambrook, et al., *supra*.

In order to clone the rhAR gene by one of the preferred methods, the amino acid sequence or DNA sequence of rhAR or a homologous protein may be necessary. To accomplish this, the rhAR protein or a homologous protein may be purified and partial amino acid sequence determined by automated sequenators or mass spectroscopy. It is not necessary to determine the entire amino acid sequence, but the linear sequence of two regions of 6 to 8 amino acids can be determined for the PCR amplification of a partial rhAR DNA fragment. Once suitable amino acid sequences have been identified, the DNA molecules capable of encoding them are synthesized. Because the genetic code is degenerate, more than one codon may be used to encode a particular amino acid, and therefore, the amino acid sequence can be encoded by any of a set of similar DNA oligonucleotides. Only one member of the set will be identical to the rhAR sequence but others in the set will be capable of hybridizing to rhAR DNA even in the presence of DNA oligonucleotides with mismatches. The mismatched DNA oligonucleotides may still sufficiently hybridize to the rhAR DNA to permit identification and isolation of rhAR encoding DNA. Alternatively, the nucleotide sequence of a region of an expressed sequence may be identified by searching one or more available genomic databases. Gene-specific primers may be used to perform PCR amplification of a cDNA of interest from either

a cDNA library or a population of cDNAs. As noted above, the appropriate nucleotide sequence for use in a PCR-based method may be obtained from SEQ ID NO: 1 or 18-20, either for the purpose of isolating overlapping 5' and 3' RACE products for generation of a full-length sequence coding for rhAR, or to isolate a portion of the nucleotide molecule coding for rhAR for use as a probe to screen one or more cDNA- or genomic-based libraries to isolate a full-length molecule encoding rhAR or rhAR-like proteins.

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In an exemplified method, the rhAR full-length cDNA of the present invention was isolated by screening template cDNA synthesized from *Macaca mulatta* prostate mRNA. Oligonucleotide primers based on *Macaca fascicularis* AR were synthesized. Template cDNA was synthesized from *Macaca mulatta* prostate mRNA. NH2 portion and COOH-portion primer pairs were used to generate two PCR fragments, which were subcloned, characterized and assembled into a full length DNA sequence (see SEQ ID NOs: 1 and 3). The cloned *Macaca mulatta* AR cDNA has 7 nucleotide differences from *Macaca fascicularis* AR in the coding region which result in two amino acid residues difference (Fig. 4). The two macaque polyQ and polyG sequences are identical to each other, and are in turn shorter than the corresponding human sequences. A single amino acid difference between the macaque and human AR, [Ala-632], is present in the DBD-Hinge-LBD region.

The present invention also relates to recombinant vectors and recombinant hosts, both prokaryotic and eukaryotic, which have been transfected and/ortransformed with the nucleic acid molecules disclosed throughout this specification.

The present invention also relates to methods of expressing rhAR and biological equivalents disclosed herein, the expressed, processed form of the protein, assays employing these recombinantly expressed gene products, cells expressing these gene products, and agonistic and/or antagonistic compounds identified through the use of assays utilizing these recombinant forms, including, but not limited to, one or more modulators of rhAR, either through direct contact with the LBD or through direct or indirect contact with a ligand which either interacts with the DBD or with the wild-type transcription complex which the androgen receptor interacts in trans, thereby modulating bone biology, for example.

The present invention relates to methods of expressing rhAR in recombinant systems and of identifying agonists and antagonists of rhAR. The novel

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rhAR proteins of the present invention are suitable for use in an assay procedure for the identification of compounds which modulate the transactivation activity of mammalian rhAR. Modulating rhAR activity, as described herein includes the inhibition or activation of this soluble transacting factor and therefore includes directly or indirectly affecting the normal regulation of the rhAR activity. Compounds that modulate rhAR include agonists, antagonists and compounds which directly or indirectly affect regulation of rhAR. When screening compounds in order to identify potential pharmaceuticals that specifically interact with a target protein, it is necessary to ensure that the compounds identified are as specific as possible for the target protein. To do this, it may necessary to screen the compounds against as wide an array as possible of proteins that are similar to the target receptor, including species homologous to rhesus androgen receptor. Thus, in order to find compounds that are potential pharmaceuticals that interact with rhAR, it is necessary not only to ensure that the compounds interact with rhAR (the "plus target") and produce the desired pharmacological effect through rhAR, it is also necessary to determine that the compounds do not interact with proteins B, C, D, etc. (the "minus targets"). In general, as part of a screening program, it is important to have as many minus targets as possible (see Hodgson, 1992, Bio/Technology 10:973-980, @ 980). rhAR proteins and the DNA molecules encoding this protein may serve this purpose in assays utilizing, for example, other members of the nuclear receptor superfamily.

As used herein, a "biologically functional derivative" of a wild-type rhAR possesses a biological activity that is related to the biological activity of the wild type rhAR. The term "functional derivative" is intended to include the "fragments," "mutants," "variants," "degenerate variants," "analogs" and "homologues" of the wild type rhAR protein. The term "fragment" is meant to refer to any polypeptide subset of wild-type rhAR, including but not necessarily limited to rhAR proteins comprising amino acid substitutions, deletions, additions, amino terminal truncations and/or carboxy-terminal truncations. The term "mutant" is meant to refer a subset of a biologically active fragment that may be substantially similar to the wild-type form but possesses distinguishing biological characteristics. Such altered characteristics include but are in no way limited to altered substrate binding, altered substrate affinity and altered sensitivity to chemical compounds affecting biological activity of the rhAR or a rhAR functional derivative. The term

"variant" is meant to refer to a molecule substantially similar in structure and function to either the wild-type protein or to a fragment thereof.

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A variety of mammalian expression vectors may be used to express recombinant rhAR in mammalian cells. Expression vectors are defined herein as DNA sequences that are required for the transcription of cloned DNA and the translation of their mRNAs in an appropriate host. Such vectors can be used to express eukaryotic DNA in a variety of hosts such as bacteria, blue green algae, plant cells, insect cells and animal cells. Specifically designed vectors allow the shuttling of DNA between hosts such as bacteria-yeast or bacteria-animal cells. An appropriately constructed expression vector should contain: an origin of replication for autonomous replication in host cells, selectable markers, a limited number of useful restriction enzyme sites, a potential for high copy number, and active promoters. A promoter is defined as a DNA sequence that directs RNA polymerase to bind to DNA and initiate RNA synthesis. A strong promoter is one that causes mRNAs to be initiated at high frequency. Expression vectors may include, but are not limited to, cloning vectors, modified cloning vectors, specifically designed plasmids or viruses.

Commercially available mammalian expression vectors which may be suitable for recombinant rhAR expression, include but are not limited to, pcDNA3.1 (Invitrogen), pLITMUS28, pLITMUS29, pLITMUS38 and pLITMUS39 (New England Bioloabs), pcDNAI, pcDNAIamp (Invitrogen), pcDNA3 (Invitrogen), pMC1neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2-neo (ATCC 37593) pBPV-1(8-2) (ATCC 37110), pdBPV-MMTneo(342-12) (ATCC 37224), pRSVgpt (ATCC 37199), pRSVneo (ATCC 37198), pSV2-dhfr (ATCC 37146), pUCTag (ATCC 37460), and IZD35 (ATCC 37565).

A variety of bacterial expression vectors may be used to express recombinant rhAR in bacterial cells. Commercially available bacterial expression vectors which may be suitable for recombinant rhAR expression include, but are not limited to pCRII (Invitrogen), pCR2.1 (Invitrogen), pQE (Qiagen), pET11a (Novagen), lambda gt11 (Invitrogen), pKK223-3 (Pharmacia), and pGEX2T (Pharmacia).

A variety of fungal cell expression vectors may be used to express recombinant rhAR in fungal cells. Commercially available fungal cell expression vectors which may be suitable for recombinant rhAR expression include but are not

limited to the ESP<sup>®</sup> yeast expression system, which utilizes *S. pombe* as the expression host, pYES2 (Invitrogen) and *Pichia* expression vector (Invitrogen).

A variety of insect cell expression vectors may be used to express recombinant receptor in insect cells. Commercially available insect cell expression vectors which may be suitable for recombinant expression of rhAR include but are not limited to pBlueBacIII and pBlueBacHis2 (Invitrogen), and pAcG2T (Pharmingen).

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An expression vector containing DNA encoding a rhAR or rhAR-like protein may be used for expression of rhAR in a recombinant host cell. Recombinant host cells may be prokaryotic or eukaryotic, including but not limited to bacteria such as *E. coli*, fungal cells such as yeast, mammalian cells including but not limited to cell lines of rhAR, bovine, porcine, monkey and rodent origin, and insect cells including but not limited to Drosophila- and silkworm-derived cell lines. Cell lines derived from mammalian species which may be suitable and which are commercially available, include but are not limited to, L cells L-M(TK-) (ATCC CCL 1.3), L cells L-M (ATCC CCL 1.2), Saos-2 (ATCC HTB-85), 293 (ATCC CRL 1573), Raji (ATCC CCL 86), CV-1 (ATCC CCL 70), COS-1 (ATCC CRL 1650), COS-7 (ATCC CRL 1651), CHO-K1 (ATCC CCL 61), 3T3 (ATCC CCL 92), NIH/3T3 (ATCC CRL 1658), HeLa (ATCC CCL 2), C127I (ATCC CRL 1616), BS-C-1 (ATCC CCL 26), MRC-5 (ATCC CCL 171) and CPAE (ATCC CCL 209).

The expression vector may be introduced into host cells via any one of a number of techniques including but not limited to transfection, transformation, protoplast fusion, and electroporation. The expression vector-containing cells are individually analyzed to determine whether they produce rhAR protein.

Identification of rhAR expressing cells may be done by several means, including but not limited to immunological reactivity with anti-rhAR antibodies, labeled ligand binding and the presence of host cell-associated rhAR activity.

The cloned rhAR cDNA obtained through the methods described above may be recombinantly expressed by molecular cloning into an expression vector (such as pcDNA3.1, pQE, pBlueBacHis2 and pLITMUS28) containing a suitable promoter and other appropriate transcription regulatory elements, and transferred into prokaryotic or eukaryotic host cells to produce recombinant rhAR. Techniques for such manipulations can be found described in Sambrook, et al., *supra* 

, are discussed at length in the Example section and are well known and easily available to the artisan of ordinary skill in the art.

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Expression of rhAR DNA may also be performed using *in vitro* produced synthetic mRNA. Synthetic mRNA can be efficiently translated in various cell-free systems, including but not limited to wheat germ extracts and reticulocyte extracts, as well as efficiently translated in cell based systems, including but not limited to microinjection into frog oocytes, with microinjection into frog oocytes being preferred.

To determine the rhAR cDNA sequence(s) that yields optimal levels of rhAR, cDNA molecules including but not limited to the following can be constructed: a cDNA fragment containing the full-length open reading frame for rhAR as well as various constructs containing portions of the cDNA encoding only specific domains of the protein or rearranged domains of the protein. All constructs can be designed to contain none, all or portions of the 5' and/or 3' untranslated region of a rhAR cDNA.

15 The expression levels and activity of rhAR can be determined following the introduction, both singly and in combination, of these constructs into appropriate host cells. Following determination of the rhAR cDNA cassette yielding optimal expression in transient assays, this rhAR cDNA construct is transferred to a variety of expression vectors (including recombinant viruses), including but not limited to those combinant cells, plant cells, insect cells, oocytes, bacteria, and yeast cells.

A preferred aspect of the present invention relates to a substantially purified form of the novel nuclear trans-acting receptor protein, a rhesus androgen receptor protein, which is disclosed in Figures 2 (SEQ ID NO:2) as well as a polymorph of the protein disclosed in SEQ ID NO:2, disclosed herein as SEQ ID NO:4.

The rhAR protein disclosed in SEQ ID NO:2 is as follows:

MEVQLGLGRV YPRPPSKTYR GAFQNLFQSV REVIQNPGPR HPEAASAAPP

GASLQQQQQQ QQETSPRQQQ QQQQGEDGSP QAHRRGPTGY LVLDEEQQPS

QPQSAPECHP ERGCVPEPGA AVAAGKGLPQ QLPAPPDEDD SAAPSTLSLL

GPTFPGLSSC SADLKDILSE ASTMQLLQQQ QQEAVSEGSS SGRAREASGA

PTSSKDNYLE GTSTISDSAK ELCKAVSVSM GLGVEALEHL SPGEQLRGDC

MYAPVLGVPP AVRPTPCAPL AECKGSLLDD SAGKSTEDTA EYSPFKGGYT

KGLEGESLGC SGSAAAGSSG TLELPSTLSL YKSGALDEAA AYQSRDYYNF

PLALAGPPPP PPPPHPHARI KLENPLDYGS AWAAAAAQCR YGDLASLHGA

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GAAGPGSGSP SAAASSSWHT LFTAEEGQLY GPCGGGGGG GGGGGAGEA
GAVAPYGYTR PPQGLAGQEG DFTAPDVWYP GGMVSRVPYP SPTCVKSEMG
PWMDSYSGPY GDMRLETARD HVLPIDYYFP PQKTCLICGD EASGCHYGAL
TCGSCKVFFK RAAEGKQKYL CASRNDCTID KFRKNCPSC RLRKCYEAGM

5 TLGARKLKKL GNLKLQEEGE ASSTTSPTEE TAQKLTVSHI EGYECQPIFL
NVLEAIEPGV VCAGHDNNQP DSFAALLSSL NELGERQLVH VVKWAKALPG
FRNLHVDDQM AVIQYSWMGL MVFAMGWRSF TNVNSRMLYF APDLVFNEYR
MHKSRMYSQC VRMRHLSQEF GWLQITPQEF LCMKALLLFS IIPVDGLKNQ
KFFDELRMNY IKELDRIIAC KRKNPTSCSR RFYQLTKLLD SVQPIARELH
10 QFTFDLLIKS HMVSVDFPEM MAEIISVQVP KILSGKVKPI YFHTQ (SEQ ID
NO:2).
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As noted herein, the Glu-210 residue (underlined and bolded) of rhAR of SEQ ID NO:2 represents an allelic variant at nucleotide 1051 of SEQ ID NO:1. A single nucleotide change at nucleotide 1051 from 'A' to 'G' results in an amino acid change at residue 210 of the rhAR, from the Glu residue of SEQ ID NO:2 to a Gly residue (underlined and bolded), shown below as SEQ ID NO:4:

MEVOLGLGRY YPRPPSKTYR GAFONLFQSV REVIQNPGPR HPEAASAAPP

GASLQQQQQ QQETSPRQQQ QQQQGEDGSP QAHRRGPTGY LVLDEEQQPS QPQSAPECHP ERGCVPEPGA AVAAGKGLPQ QLPAPPDEDD SAAPSTLSLL GPTFPGLSSC SADLKDILSE ASTMOLLOQO QQEAVSEGSS SGRAREASGA PTSSKDNYLG GTSTISDSAK ELCKAVSVSM GLGVEALEHL SPGEQLRGDC MYAPVLGVPP AVRPTPCAPL AECKGSLLDD SAGKSTEDTA EYSPFKGGYT KGLEGESLGC SGSAAAGSSG TLELPSTLSL YKSGALDEAA AYQSRDYYNF PLALAGPPPP PPPPHPHARI KLENPLDYGS AWAAAAAQCR YGDLASLHGA GAAGPGSGSP SAAASSSWHT LFTAEEGQLY GPCGGGGGGG GGGGGGAGEA GAVAPYGYTR PPQGLAGQEG DFTAPDVWYP GGMVSRVPYP SPTCVKSEMG PWMDSYSGPY GDMRLETARD HVLPIDYYFP PQKTCLICGD EASGCHYGAL TCGSCKVFFK RAAEGKQKYL CASRNDCTID KFRKNCPSC RLRKCYEAGM TLGARKLKKL GNLKLQEEGE ASSTTSPTEE TAQKLTVSHI EGYECQPIFL NVLEAIEPGV VCAGHDNNQP DSFAALLSSL NELGERQLVH VVKWAKALPG FRNLHVDDOM AVIQYSWMGL MVFAMGWRSF TNVNSRMLYF APDLVFNEYR MHKSRMYSQC VRMRHLSQEF GWLQITPQEF LCMKALLLFS IIPVDGLKNQ KFFDELRMNY IKELDRIIAC KRKNPTSCSR RFYQLTKLLD SVQPIARELH

QFTFDLLIKS HMVSVDFPEM MAEIISVQVP KILSGKVKPI YFHTQ (SEQ ID NO:4).

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The underlined portions of SEQ ID NOs:2 and 4, from amino acid residue 535 to residue 600, represent the DNA binding domain (DBD) of the rhAR receptor protein. The DBD participates in regulating protein-protein interactions in AR transrepression pathway. Aarnisalo et al., Endocrinology 140(7):3097 (1999). Transcription activation and repression functions of the androgen receptor are differentially influenced by mutations in the DNA-binding domain. In transactivation, AR forms homodimer and binds DNA response element via DBD.

The present invention also relates to a substantially purified, fully processed (including proteolytic processing, such as processing of a natural, hybrid or synthetic signal sequence, glycosylation and/or phosphorylation) mature rhAR protein obtained from a recombinant host cell containing a DNA expression vector comprising a nucleotide sequence as set forth in SEQ ID NOs: 1 and 3, or nucleic acid fragments thereof as described above, such DNA expression vectors expressing the respective rhAR protein or rhAR precursor protein. It is especially preferred that the recombinant host cell be a eukaryotic host cell, including but not limited to a mammalian cell line or an insect cell line. In another embodiment, it is especially preferred that the recombinant host cell be a yeast host cell.

The present invention also relates to isolated nucleic acid molecules which are fusion constructions expressing fusion proteins useful in assays to identify compounds which modulate mammalian AR. A preferred aspect of this portion of the invention includes, but is not limited to, glutathione S-transferase GST-rhAR fusion constructs. These fusion constructs include, but are not limited to, all or a portion of the ligand-binding domain of rhAR, respectively, as an in-frame fusion at the carboxy terminus of the GST gene. The disclosure of SEQ ID NOS:1 and 3 provide the artisan of ordinary skill the information necessary to construct any such nucleic acid molecule encoding a GST-nuclear receptor fusion protein. Soluble recombinant GST-nuclear receptor fusion proteins may be expressed in various expression systems, including but in now manner limited to a yeast expression system (see Example Section 2), or *Spodoptera frugiperda* (Sf21) within insect cells (Invitrogen) using a baculovirus expression vector (e.g., Bac-N-Blue DNA from Invitrogen or pAcG2T from Pharmingen). Example Section 2 discloses construction of GST-Flag-rhARLBD (Mr = 60 kDa), which is expressed in yeast. This fusion protein is purified

by standard techniques and used in a hydoxyapatite binding assay in the presence of labeled R1881 and unlabeled test compounds. After a parallel binding reaction where increasing concentration of unlabeled test compounds are incubated with <sup>3</sup>H-R1881, a hydroxyapatite slurry is prepared and processed. Unbound ligand is removed and the subsequent hydroxyapatite pellet is washed and ligand bound GST-rhAR is assessed to quantify the amount of radioligand (<sup>3</sup>H-R1881) bound to the recombinant rhAR fusion protein. Results are compared to known high affinity ligands such as 5-alpha dihydrotestosterone and unlabeled R1881, which exhibit IC50s of ca. 1 nM. See, Asselin and Melancon, 1977, Steroids 30: 591-604; Ghanadian et al., 1977, Urol. Res. 5(4): 169-173.

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Other assays are contemplated for the rhAR cDNA clones of the present invention, including but not limited to the use of these clone(s) to set up cotransfection assays to measure bioactivity of compounds, or to set-up mammalian two-hybrid assays to test the effect of compounds on N- and C-terminus interaction of Macaca mulatta AR.

For example, the present invention relates to constructs wherein a receptor construct (e.g., containing the rhAR LBD, e.g., Gal4-rhAR-LBD) and a reporter construct (such as SEAP or LacZ) with regulatory sites that respond to increases and decreases in expression of the receptor construct. Therefore, the present invention includes assays by which modulators of rhAR are identified. Methods for identifying agonists and antagonists of other receptors are well known in the art and can be adapted to identify compounds which effect *in vivo* levels of rhAR. Accordingly, the present invention includes a method for determining whether a substance is a potential modulator of AR levels that comprises:

- (a) transfecting or transforming cells with an expression vector encoding rhAR, (such as the LBD of rhAR) also known as the receptor vector;
  - (b) transfecting or transforming the cells of step (a) with second expression vector, also known as a reporter vector, which comprises an element known to respond to rhAR through protein-protein interactions but bind a non-rhAR protein or a promoter fragment fused upstream of a reporter gene;
  - (c) allowing the transfected cells to grow for a time sufficient for rhAR to be expressed;
  - (d) exposing some of the transfected cells expressing rhAR, the "test cells" to a test substance while not exposing control cells to the test substance;

(e) measuring the expression of the reporter gene in both the test cells and control cells.

Of course, "controls" in such assays may take many forms, such as but not limited to the recitation of step (d) above, or possibly the use of cells not transfected with the nucleic acid molecule expressing rhAR (i.e., non-transfected cells), or cells transfected with vector alone, minus the coding region for rhAR. Also, conditions under which step (d) of the method is practiced are conditions that are typically used in the art for the study of protein-ligand interactions: *e.g.*, physiological pH; salt conditions such as those represented by such commonly used buffers as PBS or in tissue culture media; a temperature of about 4°C to about 55°C. This assay may be conducted with crude cell lysate, or with more purified materials.

Alternatively, the transrepression assay may be carried out as follows:

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- (a) provide test cells by transfecting cells with a receptor expression vector that directs the expression of rhAR or a portion thereof (such as the LBD of rhAR) in the cells;
- (b) providing test cells by transfecting the cells of step (a) with a second reporter expression vector that directs expression of a reporter gene under control of a regulatory element which is responsive to rhAR via protein-protein interactions or a portion of the rhAR construct;
  - (c) exposing the test cells to the substance;
  - (d) measuring expression of the reporter gene;
- (e) comparing the amount of expression of the reporter gene in the test cells with the amount of expression of the reporter gene in control cells that have been transfected with a reporter vector of step (b) but not a receptor vector of step (a).

This assay may be conducted with transfected mammalian cell lines using cell-permeable test compounds.

An alternative assay would be one wherein multiple receptor/reporter constructs are transfected into cells such that the general nature of the trans-acting factor can be measured. It is evident that any number of variations known to one of skill in the art may be utilized in order to provide for an assay to measure the effect of a substance on the ability of the nuclear receptor proteins of the present invention to effect transcription of a promoter of interest via protein-protein interactions with heterologous DNA binding proteins.

The present invention includes additional methods for determining whether a substance is capable of binding to rhAR, i.e., whether the substance is a potential agonist or an antagonist of rhAR, where the method comprises:

(a) providing test cells by transfecting cells with an expression vector that directs the expression of rhAR in the cells;

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- (b) exposing the test cells and control cells to the substance;
- (c) measuring the amount of binding of the substance to rhAR;
- (d) comparing the amount of binding of the substance to rhAR in the test cells with the amount of binding of the substance to control cells that have not been transfected with rhAR or a portion thereof; wherein if the amount of binding of the substance is greater in the test cells as compared to the control cells, the substance is capable of binding to rhAR. Determining whether the substance is actually an agonist or antagonist can then be accomplished by the use of functional assays such as the transrepression assay as described above.

Test compounds that regulate rhAR function through gene expression may be evaluated employing the method above.

The conditions under which step (b) of the method is practiced are conditions that are typically used in the art for the study of protein-ligand interactions: e.g., physiological pH; salt conditions such as those represented by such commonly used buffers as PBS or in tissue culture media; a temperature of about 4°C to about 55°C.

The assays described above can be carried out with cells that have been transiently or stably transfected with rhAR. Transfection is meant to include any method known in the art for introducing rhAR into the test cells. For example, transfection includes calcium phosphate or calcium chloride mediated transfection, lipofection, infection with a retroviral construct containing rhAR, and electroporation. Where binding of the substance or agonist to rhAR is measured, such binding can be measured by employing a labeled substance or agonist. The substance or agonist can be labeled in any convenient manner known to the art, e.g., radioactively, fluorescently, enzymatically.

The rhAR of the present invention may be used to screen for rhAR ligands by assessing transcriptional regulation proceeding via the ligand-bound rhAR-transcription factor protein -protein interactions. Alternatively, the rhAR of the

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present invention may be employed to screen for rhAR ligands using co-transfection with classical nuclear receptor response elements that bind the rhAR DBD.

The present invention also relates to polyclonal and monoclonal antibodies raised in response to rhAR. Recombinant rhAR protein can be separated from other cellular proteins by use of an immunoaffinity column made with monoclonal or polyclonal antibodies specific for full-length rhAR protein, or polypeptide fragments of rhAR protein. Additionally, polyclonal or monoclonal antibodies may be raised against a synthetic peptide (usually from about 9 to about 25 amino acids in length) from a portion of the protein as disclosed in SEQ ID NO:2 and/or SEQ ID NO:4. Monospecific antibodies to rhAR are purified from mammalian antisera containing antibodies reactive against rhAR or are prepared as monoclonal antibodies reactive with rhAR using the technique of Kohler and Milstein (1975, Nature 256: 495-497). Monospecific antibody as used herein is defined as a single antibody species or multiple antibody species with homogenous binding characteristics for rhAR. Homogenous binding as used herein refers to the ability of the antibody species to bind to a specific antigen or epitope, such as those associated with rhAR, as described above. rhAR-specific antibodies are raised by immunizing animals such as mice, rats, guinea pigs, rabbits, goats, horses and the like, with an appropriate concentration of rhAR protein or a synthetic peptide generated from a portion of rhAR with or without an immune adjuvant.

Preimmune serum is collected prior to the first immunization. Each animal receives between about 0.1 mg and about 1000 mg of rhAR protein associated with an acceptable immune adjuvant. Such acceptable adjuvants include, but are not limited to, Freund's complete, Freund's incomplete, alum-precipitate, water in oil emulsion containing *Corynebacterium parvum* and tRNA. The initial immunization consists of rhAR protein or peptide fragment thereof in, preferably, Freund's complete adjuvant at multiple sites, either subcutaneously (SC), intraperitoneally (IP) or both. Each animal is bled at regular intervals, preferably weekly, to determine antibody titer. The animals may or may not receive booster injections following the initial immunization. Those animals receiving booster injections are generally given an equal amount of rhAR in Freund's incomplete adjuvant by the same route. Booster injections are given at about three week intervals until maximal titers are obtained. At about 7 days after each booster immunization or about weekly after a

single immunization, the animals are bled, the serum collected, and aliquots are stored at about -20°C.

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Monoclonal antibodies (mAb) reactive with rhAR are prepared by immunizing inbred mice, preferably Balb/c, with rhAR protein. The mice are immunized by the IP or SC route with about 1 mg to about 100 mg, preferably about 10 mg, of rhAR protein in about 0.5 ml buffer or saline incorporated in an equal volume of an acceptable adjuvant, as discussed above. Freund's complete adjuvant is preferred. The mice receive an initial immunization on day 0 and are rested for about 3 to about 30 weeks. Immunized mice are given one or more booster immunizations of about 1 to about 100 mg of rhAR in a buffer solution such as phosphate buffered saline by the intravenous (IV) route. Lymphocytes, from antibody positive mice, preferably splenic lymphocytes, are obtained by removing spleens from immunized mice by standard procedures known in the art. Hybridoma cells are produced by mixing the splenic lymphocytes with an appropriate fusion partner, preferably myeloma cells, under conditions that will allow the formation of stable hybridomas. Fusion partners may include, but are not limited to: mouse myelomas P3/NS1/Ag 4-1, MPC-11, S-194 and Sp 2/0, with Sp 2/0 being preferred. The antibody producing cells and myeloma cells are fused in polyethylene glycol, about 1000 mol. wt., at concentrations from about 30% to about 50%. Fused hybridoma cells are selected by growth in hypoxanthine, thymidine and aminopterin supplemented Dulbecco's Modified Eagles Medium (DMEM) by procedures known in the art. Supernatant fluids are collected form growth positive wells on about days 14, 18, and 21 and are screened for antibody production by an immunoassay such as solid phase immunoradioassay (SPIRA) using rhAR as the antigen. The culture fluids are also tested in the Ouchterlony precipitation assay to determine the isotype of the mAb. Hybridoma cells from antibody positive wells are cloned by a technique such as the soft agar technique of MacPherson, 1973, Soft Agar Techniques, in Tissue Culture Methods and Applications, Kruse and Paterson, Eds., Academic Press.

Monoclonal antibodies are produced *in vivo* by injection of pristine primed Balb/c mice, approximately 0.5 ml per mouse, with about 2 x 10<sup>6</sup> to about 6 x 10<sup>6</sup> hybridoma cells about 4 days after priming. Ascites fluid is collected at approximately 8-12 days after cell transfer and the monoclonal antibodies are purified by techniques known in the art.

In vitro production of anti-rhAR mAb is carried out by growing the hybridoma in DMEM containing about 2% fetal calf serum to obtain sufficient quantities of the specific mAb. The mAb are purified by techniques known in the art.

Antibody titers of ascites or hybridoma culture fluids are determined by various serological or immunological assays which include, but are not limited to, precipitation, passive agglutination, enzyme-linked immunosorbent antibody (ELISA) technique and radioimmunoassay (RIA) techniques. Similar assays are used to detect the presence of human rhAR in body fluids or tissue and cell extracts.

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It is readily apparent to those skilled in the art that the above-described methods for producing monospecific antibodies may be utilized to produce antibodies specific for rhAR peptide fragments, or full-length rhAR.

rhAR antibody affinity columns are made, for example, by adding the antibodies to Affigel-10 (Biorad), a gel support which is pre-activated with N-hydroxysuccinimide esters such that the antibodies form covalent linkages with the agarose gel bead support. The antibodies are then coupled to the gel via amide bonds with the spacer arm. The remaining activated esters are then quenched with 1M ethanolamine HCl (pH 8.0). The column is washed with water followed by 0.23 M glycine HCl (pH 2.6) to remove any non-conjugated antibody or extraneous protein. The column is then equilibrated in phosphate buffered saline(PBS) (pH 7.3) and the cell culture supernatants or cell extracts containing full-length rhAR or rhAR protein fragments are slowly passed through the column. The column is then washed with phosphate buffered saline until the optical density (A280) falls to background, then the protein is eluted with 0.23 M glycine-HCl (pH 2.6). The purified rhAR protein is then dialyzed against phosphate buffered saline.

Levels of rhAR in host cells are quantified by a variety of techniques including, but not limited to, immunoaffinity and/or ligand affinity techniques. rhAR-specific affinity beads or rhAR-specific antibodies are used to isolate 35S-methionine labeled or unlabelled rhAR. Labeled rhAR protein is analyzed by SDS-PAGE. Unlabelled rhAR protein is detected by Western blotting, ELISA or RIA assays employing either rhAR protein specific antibodies and/or antiphosphotyrosine antibodies.

Following expression of rhAR in a host cell, rhAR protein may be recovered to provide rhAR protein in active form. Several rhAR protein purification procedures are available and suitable for use. Recombinant rhAR protein may be

purified from cell lysates and extracts, or from conditioned culture medium, by various combinations of, or individual application of salt fractionation, ion exchange chromatography, size exclusion chromatography, hydroxylapatite adsorption chromatography and hydrophobic interaction chromatography.

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The DNA molecules, RNA molecules, recombinant protein and antibodies of the present invention may be used to screen and measure levels of rhAR. The recombinant proteins, DNA molecules, RNA molecules and antibodies lend themselves to the formulation of kits suitable for the detection and typing of rhAR. Such a kit would comprise a compartmentalized carrier suitable to hold in close confinement at least one container. The carrier would further comprise reagents such as recombinant rhAR or anti-rhAR antibodies suitable for detecting rhAR. The carrier may also contain a means for detection such as labeled antigen or enzyme substrates or the like.

Pharmaceutically useful compositions comprising modulators of rhAR may be formulated according to known methods such as by the admixture of a pharmaceutically acceptable carrier. Examples of such carriers and methods of formulation may be found in Remington's Pharmaceutical Sciences. To form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of the protein, DNA, RNA, modified rhAR, or either rhAR agonists or antagonists.

Therapeutic or diagnostic compositions comprising modulators of rhAR are administered to an individual in amounts sufficient to treat or diagnose disorders. The effective amount may vary according to a variety of factors such as the individual's condition, weight, sex and age. Other factors include the mode of administration.

The pharmaceutical compositions may be provided to the individual by a variety of routes such as subcutaneous, topical, oral and intramuscular.

The term "chemical derivative" describes a molecule that contains additional chemical moieties that are not normally a part of the base molecule. Such moieties may improve the solubility, half-life, absorption, etc. of the base molecule. Alternatively the moieties may attenuate undesirable side effects of the base molecule or decrease the toxicity of the base molecule. Examples of such moieties are described in a variety of texts, such as Remington's Pharmaceutical Sciences.

Compounds identified according to the methods disclosed herein may be used alone at appropriate dosages. Alternatively, co-administration or sequential administration of other agents may be desirable.

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The present invention also has the objective of providing suitable topical, oral, systemic and parenteral pharmaceutical formulations for use in the novel methods of treatment of the present invention. The compositions containing compounds identified according to this invention as the active ingredient can be administered in a wide variety of therapeutic dosage forms in conventional vehicles for administration. For example, the compounds can be administered in such oral dosage forms as tablets, capsules (each including timed release and sustained release formulations), pills, powders, granules, elixirs, tinctures, solutions, suspensions, syrups and emulsions, or by injection. Likewise, they may also be administered in intravenous (both bolus and infusion), intraperitoneal, subcutaneous, topical with or without occlusion, or intramuscular form, all using forms well known to those of ordinary skill in the pharmaceutical arts.

Advantageously, compounds of the present invention may be administered in a single daily dose, or the total daily dosage may be administered in divided doses of two, three or four times daily. Furthermore, compounds for the present invention can be administered in intranasal form via topical use of suitable intranasal vehicles, or via transdermal routes, using those forms of transdermal skin patches well known to those of ordinary skill in that art. To be administered in the form of a transdermal delivery system, the dosage administration will, of course, be continuous rather than intermittent throughout the dosage regimen.

For combination treatment with more than one active agent, where the active agents are in separate dosage formulations, the active agents can be administered concurrently, or they each can be administered at separately staggered times.

The dosage regimen utilizing the compounds of the present invention is selected in accordance with a variety of factors including type, species, age, weight, sex and medical condition of the patient; the severity of the condition to be treated; the route of administration; the renal, hepatic and cardiovascular function of the patient; and the particular compound thereof employed. A physician or veterinarian of ordinary skill can readily determine and prescribe the effective amount of the drug required to prevent, counter or arrest the progress of the condition. Optimal precision

in achieving concentrations of drug within the range that yields efficacy without toxicity requires a regimen based on the kinetics of the drugs availability to target sites. This involves a consideration of the distribution, equilibrium, and elimination of a drug.

The following examples are provided to illustrate the present invention without, however, limiting the same hereto.

#### **EXAMPLE 1:**

Isolation and Characterization of a DNA Molecule Encoding rhAR

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The DNA sequence for *Macaca fascicularis* monkey AR (Gen Bank Acc. # U94179, also disclosed in the attached sequence listing as SEQ ID NO:6) and an EST for *Macaca mulatta* AR (Gen Bank Accesssion No. AF092930) may be used for primer designing. The nucleotide sequence for *Macaca mulatta* AR EST is as

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TCTCAAGAGT TTGGATGGCT CCAAATCACC CCCCAGGAAT TCCTGTGCAT
GAAAGCGCTG CTACTCTTCA GCATTATTCC AGTGGATGGG CTGAAAAATC
AAAAATTCTT TGATGAACTT CGAATGAACT ACATCAAGGA ACTCGATCGT
ATCATTGCAT GCAAAAGAAA AAATCCCACA TCCTGCTCAA GGCGTTTCTA
CCAGCTCACC AAGCTCCTGG ACTCCGTGCA GCCTATTGCG AGAGAGCTGC
ATCAGTTCAC TTTTGACCTG CTAATCAAGT CACACATGGT GAGCGTGGAC
TTTCCGGAAA TGATGGCAGA GATCATCTC (SEQ ID NO:7).

Messenger RNA from rhesus monkey prostate was prepared and cDNA was synthesized by standard methods. The full-length *Macaca mulatta* AR was cloned via standard PCR methodology. Oligonucleotide primers were based on *Macaca fascicularis* AR. Template cDNA was synthesized from *Macaca mulatta* prostate mRNA. Primer pairs mkARF2 (5'-ATG GAG GTG CAG TTA GGG CTG-3'; SEQ ID NO:8) and mkARR5 (5'-GGT CTT CTG GGG TGG AAA GTA-3'; SEQ ID NO:9) were used to obtain the NH2-terminal portion of the gene via PCR, while the COOH-terminal portion was obtained using mkARF5 (5'-ACG GCT ACA CTC GGC CAC CTC-3'; SEQ ID NO:10) and mkARR2 (5'-AAC AGG CAG AAG ACA TCT GAA-3' SEQ ID NO:11). Each fragment was sub-cloned into a pCRII vector and sequencing verification was performed on DNA from each sub-clones. Clones containing wild type cDNA sequences as compared to the consensus sequence from

both NH<sub>2</sub>- and COOH- terminal DNA sequence assembly were used for full-length cDNA construction. The final full-length cDNA was obtained through ligating the 5' and the 3' end of the cDNA at a KpnI site and cloning into a pCRII vector. The nucleotide sequence was again verified via sequencing. Also, the starting Met and 5'-UTR information for *Macaca mulatta* AR was obtained through cDNA extension on subdivided *Macaca mulatta* cDNA library using mkARR7 primer (5'-GGC GGC CGA GGG TAG ACC CTC-3' SEQ ID NO:12). The cloned *Macaca mulatta* AR cDNA shows seven nucleotide differences from *Macaca fascicularis* AR in the coding region which result in two amino acid residues differences. Both open reading frames show identical polyQ and polyG sequences which are shorter than the human version, with the DBD and LBD regions being identical to the human version.

#### **EXAMPLE 2**

Generation of GST-rhAR Fusion Proteins for Use in In Vitro Screening Assays

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Expression vector construction: PCR fragment containing residues 601 to 895, which contains the whole LBD, was inserted into pESP-1 expression vector (#251600, Stratagene, Lo Jolla, CA) at SmaI site which makes the rhARLBD down stream of GST-Flag tag. The final conjunction sequences are vector 5'-GGA TCC CCC ACT CTG GGA GCC ... ... CTG CCT GTT GGG TAA-3' vector.

AR Expression - GST-Flag-rhARLBD (Mr = 60 kDa) is expressed in yeast using pESP-1 vector according to Stratagene's protocol and lysed in TEGM/DTT/PI buffer [10 mM Tris, pH7.4, 1 mM EDTA, 10% glycerol, 10 mM molybdate, 2 mM DTT, 50 ul of yeast protease inhibitor cocktail (PI: Sigma) per gram of yeast and 1/10 vol. of PI complete (PI: Boehringer-Mannheim) per gram of yeast.

Fusion Protein Purification - The above fusion protein is purified using antiflag M2 affinity gel (Sigma) via batch purification method using TEGM/DTT buffer. The protein is eluted using TEGM/DTT buffer containing 100 ug/ml of Flag peptide.

Hydroxyapatite Binding Assay - Typically, 0.25 ug/ml of recombinant purified GST-Flag-rhARLBD and 2 nM <sup>3</sup>H-R1881 are combined in 100 ul binding reaction (with 50 mM Tris, pH7.5, 10% glycerol, 0.8 M NaCl, 1 mg/ml BSA and 2 mM dithiothreitol) that is incubated for 18 hours at 4 °C. <sup>3</sup>H-R1881 binding displacement is assessed in parallel binding reaction aliquots in the presence of varying concentrations of unlabeled test compounds. Following the initial 18 hour

binding reaction, 100 ul of a 50% (wt/vol) hydroxyapatite (HAP) slurry is added to each sample, vortexed, and incubated on ice for ~ 10 min. The samples are then centrifuged and the supernatant aspirated to remove unbound ligand. The HAP pellet is washed three times with wash buffer (40 mM Tris, pH7.5, 100 mM KCl, 1 mM EDTA and 1 mM EGTA). The 3x washed HAP pellet containing ligand-bound GST-RhAR is transferred in 95% EtOH to a scintillation vial containing 5 ml scintillation fluid, mixed and counted to quantify the amount of radioligand (3H-R1881) bound to the recombinant RhAR fusion protein. Results are compared to known high affinity ligands such as 5-alpha dihydrotestosterone and unlabeled R1881, which exhibit IC50s of ca. 1 nM.

While the foregoing specification teaches the principles of the present invention, with examples provided for the purpose of illustration, it will be understood that the practice of the invention encompasses all of the usual variations, adoptions, or modifications, as come within the scope of the following claims and their equivalents.

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### WHAT IS CLAIMED:

1. A purified DNA molecule encoding a Macaca mulatta AR protein wherein said protein comprises the amino acid sequence as follows: 5 MEVQLGLGRV YPRPPSKTYR GAFQNLFQSV REVIQNPGPR HPEAASAAPP GASLOOQOOQ QQETSPRQQQ QQQQGEDGSP QAHRRGPTGY LVLDEEQQPS OPOSAPECHP ERGCVPEPGA AVAAGKGLPQ QLPAPPDEDD SAAPSTLSLL GPTFPGLSSC SADLKDILSE ASTMQLLQQQ QQEAVSEGSS SGRAREASGA PTSSKDNYLE GTSTISDSAK ELCKAVSVSM GLGVEALEHL SPGEQLRGDC 10 MYAPVLGVPP AVRPTPCAPL AECKGSLLDD SAGKSTEDTA EYSPFKGGYT KGLEGESLGC SGSAAAGSSG TLELPSTLSL YKSGALDEAA AYQSRDYYNF PLALAGPPPP PPPPHPHARI KLENPLDYGS AWAAAAAQCR YGDLASLHGA GAAGPGSGSP SAAASSSWHT LFTAEEGQLY GPCGGGGGGG GGGGGGAGEA GAVAPYGYTR PPOGLAGOEG DFTAPDVWYP GGMVSRVPYP SPTCVKSEMG 15 PWMDSYSGPY GDMRLETARD HVLPIDYYFP POKTCLICGD EASGCHYGAL TCGSCKVFFK RAAEGKOKYL CASRNDCTID KFRRKNCPSC RLRKCYEAGM TLGARKLKKL GNLKLQEEGE ASSTTSPTEE TAQKLTVSHI EGYECQPIFL NVLEAIEPGV VCAGHDNNOP DSFAALLSSL NELGERQLVH VVKWAKALPG FRNLHVDDQM AVIQYSWMGL MVFAMGWRSF TNVNSRMLYF APDLVFNEYR 20 MHKSRMYSQC VRMRHLSQEF GWLQITPQEF LCMKALLLFS IIPVDGLKNQ KFFDELRMNY IKELDRIIAC KRKNPTSCSR RFYQLTKLLD SVQPIARELH OFTFDLLIKS HMVSVDFPEM MAEIISVQVP KILSGKVKPI YFHTQ, as set forth in three-letter abbreviation in SEQ ID NO:2.

- 2. A DNA expression vector for expressing a Macaca mulatta AR protein in a recombinant host cell wherein said expression vector comprises a DNA molecule of Claim 1.
- 3. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the DNA expression vector of Claim 2.
  - 4. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:

(a) transfecting the expression vector of Claim 2 into a suitable host cell; and

(b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said DNA expression vector.

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- A purified DNA molecule encoding a Macaca mulatta AR protein wherein said protein consists of the amino acid sequence as follows: MEVOLGLGRV YPRPPSKTYR GAFONLFOSV REVIONPGPR HPEAASAAPP 10 GASLQQQQQQ QQETSPRQQQ QQQQGEDGSP QAHRRGPTGY LVLDEEQQPS QPQSAPECHP ERGCVPEPGA AVAAGKGLPQ QLPAPPDEDD SAAPSTLSLL GPTFPGLSSC SADLKDILSE ASTMQLLQQQ QQEAVSEGSS SGRAREASGA PTSSKDNYLE GTSTISDSAK ELCKAVSVSM GLGVEALEHL SPGEOLRGDC MYAPVLGVPP AVRPTPCAPL AECKGSLLDD SAGKSTEDTA EYSPFKGGYT KGLEGESLGC SGSAAAGSSG TLELPSTLSL YKSGALDEAA AYQSRDYYNF PLALAGPPPP PPPPHPHARI KLENPLDYGS AWAAAAAQCR YGDLASLHGA GAAGPGSGSP SAAASSSWHT LFTAEEGQLY GPCGGGGGGG GGGGGGAGEA GAVAPYGYTR PPQGLAGQEG DFTAPDVWYP GGMVSRVPYP SPTCVKSEMG PWMDSYSGPY GDMRLETARD HVLPIDYYFP PQKTCLICGD EASGCHYGAL 20 TCGSCKVFFK RAAEGKQKYL CASRNDCTID KFRRKNCPSC RLRKCYEAGM TLGARKLKKL GNLKLOEEGE ASSTTSPTEE TAOKLTVSHI EGYECOPIFL NVLEAIEPGV VCAGHDNNQP DSFAALLSSL NELGERQLVH VVKWAKALPG FRNLHVDDOM AVIQYSWMGL MVFAMGWRSF TNVNSRMLYF APDLVFNEYR MHKSRMYSQC VRMRHLSQEF GWLQITPQEF LCMKALLLFS IIPVDGLKNQ 25 KFFDELRMNY IKELDRIIAC KRKNPTSCSR RFYQLTKLLD SVQPIARELH OFTFDLLIKS HMVSVDFPEM MAEIISVQVP KILSGKVKPI YFHTQ, as set forth in three-letter abbreviation in SEQ ID NO:2.
- A DNA expression vector for expressing a Macaca mulatta AR
   protein in a recombinant host cell wherein said expression vector comprises a DNA molecule of Claim 5.
  - 7. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 6.

8. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:

- (a) transfecting the expression vector of Claim 6 into a suitable
- 5 host cell; and
  - (b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said expression vector.
- 9. A purified DNA molecule encoding a Macaca mulatta AR 10 protein wherein said DNA molecule comprises the nucleotide sequence, as follows: CCCAAAAAT AAAAACAAAC AAAAACAAAA CAAAACAAAA AAAACGAATA AAGAAAAGG TAATAACTCA GTTCTTATTT GCACCTACTT CCAGTGGACA CTGAATTTGG AAGGTGGAGG ATTCTTGTTT TTTCTTTTAA GATCGGGCAT CTTTTGAATC TACCCCTCAA GTGTTAAGAG ACAGACTGTG AGCCTAGCAG 15 GGCAGATCTT GTCCACCGTG TGTCTTCTTT TGCAGGAGAC TTTGAGGCTG TCAGAGCGCT TTTTGCGTGG TTGCTCCCGC AAGTTTCCTT CTCTGGAGCT TCCCGCAGGT GGGCAGCTAG CTGCAGCGAC TACCGCATCA TCACAGCCTG TTGAACTCTT CTGAGCAAGA GAAGGGGAGG CGGGGTAAGG GAAGTAGGTG GAAGATTCAG CCAAGCTCAA GGATGGAGGT GCAGTTAGGG CTGGGGAGGG 20 TCTACCCTCG GCCGCCGTCC AAGACCTACC GAGGAGCTTT CCAGAATCTG TTCCAGAGCG TGCGCGAAGT GATCCAGAAC CCGGGCCCCA GGCACCCAGA GGCCGCGAGC GCAGCACCTC CCGGCGCCAG TTTGCAGCAG CAGCAGCAGC AGCAGCAAGA AACTAGCCCC CGGCAACAGC AGCAGCAGCA GCAGGGTGAG GATGGTTCTC CCCAAGCCCA TCGTAGAGGC CCCACAGGCT ACCTGGTCCT GGATGAGGAA CAGCAGCCTT CACAGCCTCA GTCAGCCCCG GAGTGCCACC 25 CCGAGAGAGG TTGCGTCCCA GAGCCTGGAG CCGCCGTGGC CGCCGGCAAG GGGCTGCCGC AGCAGCTGCC AGCACCTCCG GACGAGGATG ACTCAGCTGC CCCATCCACG TTGTCTCTGC TGGGCCCCAC TTTCCCCGGC TTAAGCAGCT GCTCCGCCGA CCTTAAAGAC ATCCTGAGCG AGGCCAGCAC CATGCAACTC 30 CTTCAGCAAC AGCAGCAGGA AGCAGTATCC GAAGGCAGCA GCAGCGGGAG AGCGAGGGAG GCCTCGGGGG CTCCCACTTC CTCCAAGGAC AATTACTTAG AGGGCACTTC GACCATTTCT GACAGCGCCA AGGAGCTGTG TAAGGCAGTG TCGGTGTCCA TGGGCTTGGG TGTGGAGGCG TTGGAGCATC TGAGTCCAGG

GGAACAGCTT CGGGGGGATT GCATGTACGC CCCAGTTTTG GGAGTTCCAC

|    | CCGCTGTGCG | TCCCACTCCG         | TGTGCCCCAT         | TGGCCGAATG         | CAAAGGTTCT |
|----|------------|--------------------|--------------------|--------------------|------------|
|    | CTGCTAGACG | ACAGCGCAGG         | CAAGAGCACT         | GAAGATACTG         | CTGAGTATTC |
|    | CCCTTTCAAG | GGAGGTTACA         | CCAAAGGGCT         | AGAAGGCGAG         | AGCCTAGGCT |
|    | GCTCTGGCAG | CGCTGCAGCA         | GGGAGCTCCG         | GGACACTTGA         | ACTGCCGTCC |
| 5  | ACCCTGTCTC | TCTACAAGTC         | CGGAGCACTG         | GACGAGGCAG         | CTGCGTACCA |
|    | GAGTCGCGAC | TACTACAACT         | TTCCACTGGC         | TCTGGCCGGG         | CCGCCGCCC  |
|    | CTCCACCGCC | TCCCCATCCC         | CACGCTCGCA         | TCAAGCTGGA         | GAACCCGCTG |
|    | GACTATGGCA | GCGCCTGGGC         | GGCTGCGGCG         | GCGCAGTGCC         | GCTATGGGGA |
|    | CCTGGCGAGC | CTGCATGGCG         | CGGGTGCAGC         | GGGACCCGGC         | TCTGGGTCAC |
| 10 | CCTCAGCGGC | ${\tt CGCTTCCTCA}$ | TCCTGGCACA         | ${\tt CTCTCTTCAC}$ | AGCCGAAGAA |
|    | GGCCAGTTGT | ATGGACCGTG         | ${\tt TGGTGGTGGG}$ | GGCGGCGGCG         | GTGGCGGCGG |
|    | CGGCGGCGGC | GCAGGCGAGG         | ${\tt CGGGAGCTGT}$ | AGCCCCCTAC         | GGCTACACTC |
|    | GGCCACCTCA | GGGGCTGGCG         | GGCCAGGAAG         | GCGACTTCAC         | CGCACCTGAT |
|    | GTGTGGTACC | ${\tt CTGGCGGCAT}$ | GGTGAGCAGA         | $\tt GTGCCCTATC$   | CCAGTCCCAC |
| 15 | TTGTGTCAAA | AGCGAGATGG         | GCCCTGGAT          | GGATAGCTAC         | TCCGGACCTT |
|    | ACGGGGACAT | GCGTTTGGAG         | ACTGCCAGGG         | ACCATGTTTT         | GCCAATTGAC |
|    | TATTACTTTC | CACCCCAGAA         | GACCTGCCTG         | ATCTGTGGAG         | ATGAAGCTTC |
|    | TGGGTGTCAC | TATGGAGCTC         | ${\tt TCACATGTGG}$ | AAGCTGCAAG         | GTCTTCTTCA |
|    | AAAGAGCCGC | TGAAGGGAAA         | CAGAAGTACC         | ${\tt TGTGTGCCAG}$ | CAGAAATGAT |
| 20 | TGCACTATTG | ATAAATTCCG         | AAGGAAAAAT         | ${\tt TGTCCATCTT}$ | GCCGTCTTCG |
|    | GAAATGTTAT | GAAGCAGGGA         | TGACTCTGGG         | AGCCCGGAAG         | CTGAAGAAAC |
|    | TTGGTAATCT | GAAACTACAG         | GAGGAAGGAG         | AGGCTTCCAG         | CACCACCAGC |
|    | CCCACTGAGG | AGACAGCCCA         | GAAGCTGACA         | GTGTCACACA         | TTGAAGGCTA |
|    | TGAATGTCAG | CCCATCTTTC         | TGAATGTCCT         | GGAGGCCATT         | GAGCCAGGTG |
| 25 | TGGTGTGTGC | TGGACATGAC         | AACAACCAGC         | CCGACTCCTT         | CGCAGCCTTG |
|    | CTCTCTAGCC | ${\tt TCAATGAACT}$ | GGGAGAGAGA         | CAGCTTGTAC         | ATGTGGTCAA |
|    | GTGGGCCAAG | GCCTTGCCTG         | GCTTCCGCAA         | CTTACACGTG         | GACGACCAGA |
|    | TGGCTGTCAT | TCAGTACTCC         | TGGATGGGGC         | TCATGGTGTT         | TGCCATGGGC |
|    | TGGCGATCCT | TCACCAATGT         | CAACTCCAGG         | ATGCTCTACT         | TTGCCCCTGA |
| 30 | TCTGGTTTTC | AATGAGTACC         | GCATGCACAA         | ATCCCGGATG         | TACAGCCAGT |
|    | GTGTCCGAAT | GAGGCACCTC         | TCTCAAGAGT         | ${\tt TTGGATGGCT}$ | CCAAATCACC |
|    | CCCCAGGAAT | TCCTGTGCAT         | GAAAGCGCTG         | CTACTCTTCA         | GCATTATTCC |
|    | AGTGGATGGG | CTGAAAAATC         | AAAAATTCTT         | TGATGAACTT         | CGAATGAACT |
|    | ACATCAAGGA | ACTCGATCGT         | ATCATTGCAT         | GCAAAAGAAA         | AAATCCCACA |

TCCTGCTCAA GGCGTTTCTA CCAGCTCACC AAGCTCCTGG ACTCCGTGCA
GCCTATTGCG AGAGAGCTGC ATCAGTTCAC TTTTGACCTG CTAATCAAGT
CACACATGGT GAGCGTGGAC TTTCCGGAAA TGATGGCAGA GATCATCTCT
GTGCAAGTGC CCAAGATCCT TTCTGGGAAA GTCAAGCCCA TCTATTTCCA
CACCCAGTGA AGCATTGGAA ATCCCTATTT CCTCACCCCA GCTCATGCCC
CCTTTCAGAT GTCTTCTGCC TGTTA, set forth as SEQ ID NO:1.

- 10. A DNA molecule of Claim 9 which consists of nucleotide 154 to about nucleotide 1257 of SEQ ID NO: 1.
- 11. An expression vector for expressing a Macaca mulatta AR protein wherein said expression vector comprises a DNA molecule of Claim 9.

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- 12. An expression vector for expressing a Macaca mulatta AR protein wherein said expression vector comprises a DNA molecule of Claim 10.
  - 13. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 11.
- 20 14. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 12.
  - 15. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:
- 25 (a) transfecting the expression vector of Claim 11 into a suitable host cell; and,
  - (b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said expression vector.
- 30 16. The process of Claim 15 wherein the host cell is a yeast host cell.
  - 17. A purified DNA molecule encoding a Macaca mulatta AR protein wherein said DNA molecule consists of the nucleotide sequence, as follows,

|    | CCCAAAAAAT                           | AAAAACAAAC         | АААААСАААА         | CAAAACAAAA         | AAAACGAATA         |
|----|--------------------------------------|--------------------|--------------------|--------------------|--------------------|
|    | AAGAAAAAGG                           | TAATAACTCA         | ${\tt GTTCTTATTT}$ | GCACCTACTT         | CCAGTGGACA         |
|    | CTGAATTTGG                           | AAGGTGGAGG         | ATTCTTGTTT         | ${\tt TTTCTTTTAA}$ | GATCGGGCAT         |
|    | CTTTTGAATC                           | TACCCCTCAA         | GTGTTAAGAG         | ACAGACTGTG         | AGCCTAGCAG         |
| 5  | GGCAGATCTT                           | GTCCACCGTG         | TGTCTTCTTT         | TGCAGGAGAC         | TTTGAGGCTG         |
|    | TCAGAGCGCT                           | TTTTGCGTGG         | TTGCTCCCGC         | AAGTTTCCTT         | CTCTGGAGCT         |
|    | TCCCGCAGGT                           | GGGCAGCTAG         | CTGCAGCGAC         | TACCGCATCA         | TCACAGCCTG         |
|    | TTGAACTCTT                           | CTGAGCAAGA         | GAAGGGGAGG         | CGGGGTAAGG         | GAAGTAGGTG         |
|    | GAAGATTCAG                           | CCAAGCTCAA         | GGATGGAGGT         | GCAGTTAGGG         | CTGGGGAGGG         |
| 10 | TCTACCCTCG                           | GCCGCCGTCC         | AAGACCTACC         | GAGGAGCTTT         | CCAGAATCTG         |
|    | TTCCAGAGCG                           | TGCGCGAAGT         | GATCCAGAAC         | CCGGGCCCCA         | GGCACCCAGA         |
|    | GGCCGCGAGC                           | GCAGCACCTC         | CCGGCGCCAG         | TTTGCAGCAG         | CAGCAGCAGC         |
|    | AGCAGCAAGA                           | AACTAGCCCC         | CGGCAACAGC         | AGCAGCAGCA         | GCAGGGTGAG         |
|    | GATGGTTCTC                           | CCCAAGCCCA         | TCGTAGAGGC         | CCCACAGGCT         | ACCTGGTCCT         |
| 15 | GGATGAGGAA                           | CAGCAGCCTT         | CACAGCCTCA         | GTCAGCCCCG         | GAGTGCCACC         |
|    | CCGAGAGAGG                           | ${\tt TTGCGTCCCA}$ | GAGCCTGGAG         | CCGCCGTGGC         | CGCCGGCAAG         |
|    | GGGCTGCCGC                           | AGCAGCTGCC         | AGCACCTCCG         | GACGAGGATG         | ACTCAGCTGC         |
|    | CCCATCCACG                           | ${\tt TTGTCTCTGC}$ | TGGGCCCCAC         | TTTCCCCGGC         | ${\tt TTAAGCAGCT}$ |
|    | GCTCCGCCGA                           | CCTTAAAGAC         | ATCCTGAGCG         | AGGCCAGCAC         | CATGCAACTC         |
| 20 | CTTCAGCAAC                           | AGCAGCAGGA         | AGCAGTATCC         | GAAGGCAGCA         | GCAGCGGGAG         |
|    | AGCGAGGGAG                           | GCCTCGGGGG         | ${\tt CTCCCACTTC}$ | CTCCAAGGAC         | AATTACTTAG         |
|    | $\underline{\underline{AGGGCACTTC}}$ | GACCATTTCT         | GACAGCGCCA         | AGGAGCTGTG         | TAAGGCAGTG         |
|    | TCGGTGTCCA                           | TGGGCTTGGG         | TGTGGAGGCG         | TTGGAGCATC         | TGAGTCCAGG         |
|    | GGAACAGCTT                           | CGGGGGGATT         | GCATGTACGC         | CCCAGTTTTG         | GGAGTTCCAC         |
| 25 | CCGCTGTGCG                           | TCCCACTCCG         | TGTGCCCCAT         | ${\tt TGGCCGAATG}$ | CAAAGGTTCT         |
|    | CTGCTAGACG                           | ACAGCGCAGG         | CAAGAGCACT         | GAAGATACTG         | CTGAGTATTC         |
|    | CCCTTTCAAG                           | GGAGGTTACA         | CCAAAGGGCT         | AGAAGGCGAG         | AGCCTAGGCT         |
|    | GCTCTGGCAG                           | CGCTGCAGCA         | GGGAGCTCCG         | GGACACTTGA         | ACTGCCGTCC         |
|    | ACCCTGTCTC                           | TCTACAAGTC         | CGGAGCACTG         | GACGAGGCAG         | CTGCGTACCA         |
| 30 | GAGTCGCGAC                           | TACTACAACT         | ${\tt TTCCACTGGC}$ | TCTGGCCGGG         | CCGCCGCCCC         |
|    | CTCCACCGCC                           | TCCCCATCCC         | CACGCTCGCA         | TCAAGCTGGA         | GAACCCGCTG         |
|    | GACTATGGCA                           | GCGCCTGGGC         | GGCTGCGGCG         | GCGCAGTGCC         | GCTATGGGGA         |
|    | CCTGGCGAGC                           | CTGCATGGCG         | CGGGTGCAGC         | GGGACCCGGC         | TCTGGGTCAC         |
|    | CCTCAGCGGC                           | CGCTTCCTCA         | TCCTGGCACA         | CTCTCTTCAC         | AGCCGAAGAA         |

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GGCCAGTTGT ATGGACCGTG TGGTGGTGGG GGCGCGGCG GTGGCGGCGG
    CGGCGGCGC GCAGGCGAGG CGGGAGCTGT AGCCCCCTAC GGCTACACTC
    GGCCACCTCA GGGGCTGGCG GGCCAGGAAG GCGACTTCAC CGCACCTGAT
    GTGTGGTACC CTGGCGGCAT GGTGAGCAGA GTGCCCTATC CCAGTCCCAC
 5
    TTGTGTCAAA AGCGAGATGG GCCCCTGGAT GGATAGCTAC TCCGGACCTT
    ACGGGGACAT GCGTTTGGAG ACTGCCAGGG ACCATGTTTT GCCAATTGAC
    TATTACTTTC CACCCCAGAA GACCTGCCTG ATCTGTGGAG ATGAAGCTTC
    TGGGTGTCAC TATGGAGCTC TCACATGTGG AAGCTGCAAG GTCTTCTTCA
    AAAGAGCCGC TGAAGGGAAA CAGAAGTACC TGTGTGCCAG CAGAAATGAT
10
    TGCACTATTG ATAAATTCCG AAGGAAAAAT TGTCCATCTT GCCGTCTTCG
    GAAATGTTAT GAAGCAGGGA TGACTCTGGG AGCCCGGAAG CTGAAGAAAC
    TTGGTAATCT GAAACTACAG GAGGAAGGAG AGGCTTCCAG CACCACCAGC
    CCCACTGAGG AGACAGCCCA GAAGCTGACA GTGTCACACA TTGAAGGCTA
    TGAATGTCAG CCCATCTTTC TGAATGTCCT GGAGGCCATT GAGCCAGGTG
15
    TGGTGTGTGC TGGACATGAC AACAACCAGC CCGACTCCTT CGCAGCCTTG
    CTCTCTAGCC TCAATGAACT GGGAGAGAGA CAGCTTGTAC ATGTGGTCAA
    GTGGGCCAAG GCCTTGCCTG GCTTCCGCAA CTTACACGTG GACGACCAGA
    TGGCTGTCAT TCAGTACTCC TGGATGGGGC TCATGGTGTT TGCCATGGGC
    TGGCGATCCT TCACCAATGT CAACTCCAGG ATGCTCTACT TTGCCCCTGA
    TCTGGTTTTC AATGAGTACC GCATGCACAA ATCCCGGATG TACAGCCAGT
20
    GTGTCCGAAT GAGGCACCTC TCTCAAGAGT TTGGATGGCT CCAAATCACC
    CCCCAGGAAT TCCTGTGCAT GAAAGCGCTG CTACTCTTCA GCATTATTCC
    AGTGGATGGG CTGAAAAATC AAAAATTCTT TGATGAACTT CGAATGAACT
    ACATCAAGGA ACTCGATCGT ATCATTGCAT GCAAAAGAAA AAATCCCACA
25
    TCCTGCTCAA GGCGTTTCTA CCAGCTCACC AAGCTCCTGG ACTCCGTGCA
    GCCTATTGCG AGAGAGCTGC ATCAGTTCAC TTTTGACCTG CTAATCAAGT
    CACACATGGT GAGCGTGGAC TTTCCGGAAA TGATGGCAGA GATCATCTCT
    GTGCAAGTGC CCAAGATCCT TTCTGGGAAA GTCAAGCCCA TCTATTTCCA
    CACCCAGTGA AGCATTGGAA ATCCCTATTT CCTCACCCCA GCTCATGCCC
30
    CCTTTCAGAT GTCTTCTGCC TGTTA, as set forth in SEQ ID NO: 1.
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18. A DNA molecule of Claim 17 which consists of nucleotide 423 to about nucleotide 3108 of SEQ ID NO: 1.

19. A DNA expression vector for expressing a Macaca mulatta AR protein wherein said expression vector comprises a DNA molecule of Claim 17.

- A DNA expression vector for expressing a Macaca mulatta
   AR protein wherein said expression vector comprises a DNA molecule of Claim 18.
  - 21. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 19.
- 10 22. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 20.
  - 23. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:
- 15 (a) transfecting the expression vector of Claim 19 into a suitable host cell; and
  - (b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said expression vector.
- 20 24. The process of Claim 23 wherein the host cell is a yeast host cell.

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- 25. A purified Macaca mulatta AR protein which comprises the amino acid sequence as set forth in SEQ ID NO: 2.
- 26. A purified Macaca mulatta AR protein which consists of the amino acid sequence as set forth in SEQ ID NO: 2.
- 27. A purified Macaca mulatta AR protein derived from a host cell transfected with a DNA expression vector which comprises the nucleotide sequence as set forth in SEQ ID NO:1.

28. A purified Macaca mulatta AR protein of Claim 27 wherein said DNA expression vector contains from about nucleotide 423 to about nucleotide 3108 of SEQ ID NO:1.

5 29. A purified DNA molecule encoding a Macaca mulatta AR protein wherein said protein comprises the amino acid sequence as follows: MEVOLGLGRV YPRPPSKTYR GAFQNLFQSV REVIQNPGPR HPEAASAAPP GASLQQQQQ QQETSPRQQQ QQQQGEDGSP QAHRRGPTGY LVLDEEQQPS OPOSAPECHP ERGCVPEPGA AVAAGKGLPO OLPAPPDEDD SAAPSTLSLL 10 GPTFPGLSSC SADLKDILSE ASTMQLLQQQ QQEAVSEGSS SGRAREASGA PTSSKDNYLG GTSTISDSAK ELCKAVSVSM GLGVEALEHL SPGEQLRGDC MYAPVLGVPP AVRPTPCAPL AECKGSLLDD SAGKSTEDTA EYSPFKGGYT KGLEGESLGC SGSAAAGSSG TLELPSTLSL YKSGALDEAA AYQSRDYYNF PLALAGPPPP PPPPHPHARI KLENPLDYGS AWAAAAAQCR YGDLASLHGA 15 GAAGPGSGSP SAAASSSWHT LFTAEEGQLY GPCGGGGGGG GGGGGGAGEA GAVAPYGYTR PPQGLAGQEG DFTAPDVWYP GGMVSRVPYP SPTCVKSEMG PWMDSYSGPY GDMRLETARD HVLPIDYYFP PQKTCLICGD EASGCHYGAL TCGSCKVFFK RAAEGKQKYL CASRNDCTID KFRRKNCPSC RLRKCYEAGM TLGARKLKKL GNLKLOEEGE ASSTTSPTEE TAOKLTVSHI EGYECOPIFL 20 NVLEAIEPGV VCAGHDNNQP DSFAALLSSL NELGERQLVH VVKWAKALPG FRNLHVDDQM AVIQYSWMGL MVFAMGWRSF TNVNSRMLYF APDLVFNEYR MHKSRMYSQC VRMRHLSQEF GWLQITPQEF LCMKALLLFS IIPVDGLKNQ KFFDELRMNY IKELDRIIAC KRKNPTSCSR RFYQLTKLLD SVQPIARELH OFTFDLLIKS HMVSVDFPEM MAEIISVQVP KILSGKVKPI YFHTQ, as set forth in 25 three-letter abbreviation in SEQ ID NO:4.

30. A DNA expression vector for expressing a Macaca mulatta AR protein in a recombinant host cell wherein said expression vector comprises a DNA molecule of Claim 29.

30

31. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the DNA expression vector of Claim 30.

32. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:

- (a) transfecting the expression vector of Claim 30 into a suitable host cell; and
- 5 (b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said DNA expression vector.
- The process according to Claim 32 wherein the host cell is a yeast host cell.
- 34. A purified DNA molecule encoding a Macaca mulatta AR protein wherein said protein consists of the amino acid sequence as follows: MEVQLGLGRV YPRPPSKTYR GAFQNLFQSV REVIQNPGPR HPEAASAAPP 15 GASLQQQQQQ QQETSPRQQQ QQQQGEDGSP QAHRRGPTGY LVLDEEQQPS QPQSAPECHP ERGCVPEPGA AVAAGKGLPQ QLPAPPDEDD SAAPSTLSLL GPTFPGLSSC SADLKDILSE ASTMQLLQQQ QQEAVSEGSS SGRAREASGA PTSSKDNYLG GTSTISDSAK ELCKAVSVSM GLGVEALEHL SPGEQLRGDC MYAPVLGVPP AVRPTPCAPL AECKGSLLDD SAGKSTEDTA EYSPFKGGYT 20 KGLEGESLGC SGSAAAGSSG TLELPSTLSL YKSGALDEAA AYQSRDYYNF PLALAGPPPP PPPPHPHARI KLENPLDYGS AWAAAAAQCR YGDLASLHGA GAAGPGSGSP SAAASSSWHT LFTAEEGQLY GPCGGGGGGG GGGGGGAGEA GAVAPYGYTR PPQGLAGQEG DFTAPDVWYP GGMVSRVPYP SPTCVKSEMG PWMDSYSGPY GDMRLETARD HVLPIDYYFP POKTCLICGD EASGCHYGAL 25 TCGSCKVFFK RAAEGKQKYL CASRNDCTID KFRRKNCPSC RLRKCYEAGM TLGARKLKKL GNLKLQEEGE ASSTTSPTEE TAQKLTVSHI EGYECQPIFL NVLEAIEPGV VCAGHDNNQP DSFAALLSSL NELGERQLVH VVKWAKALPG FRNLHVDDQM AVIQYSWMGL MVFAMGWRSF TNVNSRMLYF APDLVFNEYR MHKSRMYSQC VRMRHLSQEF GWLQITPQEF LCMKALLLFS IIPVDGLKNQ 30 KFFDELRMNY IKELDRIIAC KRKNPTSCSR RFYQLTKLLD SVQPIARELH QFTFDLLIKS HMVSVDFPEM MAEIISVQVP KILSGKVKPI YFHTQ, as set forth in three-letter abbreviation in SEQ ID NO:4.

35. A DNA expression vector for expressing a Macaca mulatta AR protein in a recombinant host cell wherein said expression vector comprises a DNA molecule of Claim 34.

- 5 36. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 35.
  - 37. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:
- 10 (a) transfecting the expression vector of Claim 35 into a suitable host cell; and
  - (b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said expression vector.
- 15 38. The process according to Claim 37 wherein the host cell is a yeast host cell.
  - 39. A purified DNA molecule encoding a Macaca mulatta AR protein wherein said DNA molecule comprises the nucleotide sequence, as follows:
- 20 CCCAAAAAT AAAAACAAAC AAAAACAAAA CAAAACAAAA AAAACGAATA
  - AAGAAAAGG TAATAACTCA GTTCTTATTT GCACCTACTT CCAGTGGACA
  - CTGAATTTGG AAGGTGGAGG ATTCTTGTTT TTTCTTTTAA GATCGGGCAT
  - CTTTTGAATC TACCCCTCAA GTGTTAAGAG ACAGACTGTG AGCCTAGCAG
  - GGCAGATCTT GTCCACCGTG TGTCTTCTTT TGCAGGAGAC TTTGAGGCTG
  - TCAGAGCGCT TTTTGCGTGG TTGCTCCCGC AAGTTTCCTT CTCTGGAGCT

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- TCCCGCAGGT GGGCAGCTAG CTGCAGCGAC TACCGCATCA TCACAGCCTG
- TTGAACTCTT CTGAGCAAGA GAAGGGGAGG CGGGGTAAGG GAAGTAGGTG
- GAAGATTCAG CCAAGCTCAA GGATGGAGGT GCAGTTAGGG CTGGGGAGGG
- TCTACCCTCG GCCGCCGTCC AAGACCTACC GAGGAGCTTT CCAGAATCTG
- TTCCAGAGCG TGCGCGAAGT GATCCAGAAC CCGGGCCCCA GGCACCCAGA
- GGCCGCGAGC GCAGCACCTC CCGGCGCCAG TTTGCAGCAG CAGCAGCAGC
- AGCAGCAAGA AACTAGCCCC CGGCAACAGC AGCAGCAGCA GCAGGGTGAG
- GATGGTTCTC CCCAAGCCCA TCGTAGAGGC CCCACAGGCT ACCTGGTCCT
- GGATGAGGAA CAGCAGCCTT CACAGCCTCA GTCAGCCCCG GAGTGCCACC

|    | CCGAGAGAGG | TTGCGTCCCA | GAGCCTGGAG         | CCGCCGTGGC         | CGCCGGCAAG |
|----|------------|------------|--------------------|--------------------|------------|
|    | GGGCTGCCGC | AGCAGCTGCC | AGCACCTCCG         | GACGAGGATG         | ACTCAGCTGC |
|    | CCCATCCACG | TTGTCTCTGC | TGGGCCCCAC         | TTTCCCCGGC         | TTAAGCAGCT |
|    | GCTCCGCCGA | CCTTAAAGAC | ATCCTGAGCG         | AGGCCAGCAC         | CATGCAACTC |
| 5  | CTTCAGCAAC | AGCAGCAGGA | AGCAGTATCC         | GAAGGCAGCA         | GCAGCGGGAG |
|    | AGCGAGGGAG | GCCTCGGGGG | CTCCCACTTC         | CTCCAAGGAC         | AATTACTTAG |
|    | GGGGCACTTC | GACCATTTCT | GACAGCGCCA         | AGGAGCTGTG         | TAAGGCAGTG |
|    | TCGGTGTCCA | TGGGCTTGGG | TGTGGAGGCG         | TTGGAGCATC         | TGAGTCCAGG |
|    | GGAACAGCTT | CGGGGGGATT | GCATGTACGC         | CCCAGTTTTG         | GGAGTTCCAC |
| 10 | CCGCTGTGCG | TCCCACTCCG | TGTGCCCCAT         | ${\tt TGGCCGAATG}$ | CAAAGGTTCT |
|    | CTGCTAGACG | ACAGCGCAGG | CAAGAGCACT         | GAAGATACTG         | CTGAGTATTC |
|    | CCCTTTCAAG | GGAGGTTACA | CCAAAGGGCT         | AGAAGGCGAG         | AGCCTAGGCT |
|    | GCTCTGGCAG | CGCTGCAGCA | GGGAGCTCCG         | ${\tt GGACACTTGA}$ | ACTGCCGTCC |
|    | ACCCTGTCTC | TCTACAAGTC | CGGAGCACTG         | GACGAGGCAG         | CTGCGTACCA |
| 15 | GAGTCGCGAC | TACTACAACT | ${\tt TTCCACTGGC}$ | ${\tt TCTGGCCGGG}$ | CCGCCGCCCC |
|    | CTCCACCGCC | TCCCCATCCC | CACGCTCGCA         | ${\tt TCAAGCTGGA}$ | GAACCCGCTG |
|    | GACTATGGCA | GCGCCTGGGC | GGCTGCGGCG         | $\tt GCGCAGTGCC$   | GCTATGGGGA |
|    | CCTGGCGAGC | CTGCATGGCG | CGGGTGCAGC         | GGGACCCGGC         | TCTGGGTCAC |
|    | CCTCAGCGGC | CGCTTCCTCA | TCCTGGCACA         | CTCTCTTCAC         | AGCCGAAGAA |
| 20 | GGCCAGTTGT | ATGGACCGTG | TGGTGGTGGG         | GGCGGCGGCG         | GTGGCGGCGG |
|    | CGGCGGCGGC | GCAGGCGAGG | ${\tt CGGGAGCTGT}$ | AGCCCCCTAC         | GGCTACACTC |
|    | GGCCACCTCA | GGGGCTGGCG | GGCCAGGAAG         | GCGACTTCAC         | CGCACCTGAT |
|    | GTGTGGTACC | CTGGCGGCAT | GGTGAGCAGA         | GTGCCCTATC         | CCAGTCCCAC |
|    | TTGTGTCAAA | AGCGAGATGG | GCCCTGGAT          | GGATAGCTAC         | TCCGGACCTT |
| 25 | ACGGGGACAT | GCGTTTGGAG | ACTGCCAGGG         | ACCATGTTTT         | GCCAATTGAC |
|    | TATTACTTTC | CACCCCAGAA | GACCTGCCTG         | ATCTGTGGAG         | ATGAAGCTTC |
|    | TGGGTGTCAC | TATGGAGCTC | TCACATGTGG         | AAGCTGCAAG         | GTCTTCTTCA |
|    | AAAGAGCCGC | TGAAGGGAAA | CAGAAGTACC         | TGTGTGCCAG         | CAGAAATGAT |
|    | TGCACTATTG | ATAAATTCCG | AAGGAAAAAT         | TGTCCATCTT         | GCCGTCTTCG |
| 30 | GAAATGTTAT | GAAGCAGGGA | TGACTCTGGG         | AGCCCGGAAG         | CTGAAGAAAC |
|    | TTGGTAATCT | GAAACTACAG | GAGGAAGGAG         | AGGCTTCCAG         | CACCACCAGC |
|    | CCCACTGAGG | AGACAGCCCA | GAAGCTGACA         | GTGTCACACA         | TTGAAGGCTA |
|    | TGAATGTCAG | CCCATCTTTC | TGAATGTCCT         | GGAGGCCATT         | GAGCCAGGTG |
|    | TGGTGTGTGC | TGGACATGAC | AACAACCAGC         | CCGACTCCTT         | CGCAGCCTTG |

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CTCTCTAGCC TCAATGAACT GGGAGAGAGA CAGCTTGTAC ATGTGGTCAA
    GTGGGCCAAG GCCTTGCCTG GCTTCCGCAA CTTACACGTG GACGACCAGA
    TGGCTGTCAT TCAGTACTCC TGGATGGGGC TCATGGTGTT TGCCATGGGC
    TGGCGATCCT TCACCAATGT CAACTCCAGG ATGCTCTACT TTGCCCCTGA
5
    TCTGGTTTTC AATGAGTACC GCATGCACAA ATCCCGGATG TACAGCCAGT
    GTGTCCGAAT GAGGCACCTC TCTCAAGAGT TTGGATGGCT CCAAATCACC
    CCCCAGGAAT TCCTGTGCAT GAAAGCGCTG CTACTCTTCA GCATTATTCC
    AGTGGATGGG CTGAAAAATC AAAAATTCTT TGATGAACTT CGAATGAACT
    ACATCAAGGA ACTCGATCGT ATCATTGCAT GCAAAAGAAA AAATCCCACA
    TCCTGCTCAA GGCGTTTCTA CCAGCTCACC AAGCTCCTGG ACTCCGTGCA
10
    GCCTATTGCG AGAGAGCTGC ATCAGTTCAC TTTTGACCTG CTAATCAAGT
    CACACATGGT GAGCGTGGAC TTTCCGGAAA TGATGGCAGA GATCATCTCT
    GTGCAAGTGC CCAAGATCCT TTCTGGGAAA GTCAAGCCCA TCTATTTCCA
    CACCCAGTGA AGCATTGGAA ATCCCTATTT CCTCACCCCA GCTCATGCCC
    CCTTTCAGAT GTCTTCTGCC TGTTA, set forth as SEQ ID NO:3.
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- 40. A DNA molecule of Claim 39 which consists of nucleotide 154 to about nucleotide 1257 of SEQ ID NO: 3.
- 20 41. An expression vector for expressing a Macaca mulatta AR protein wherein said expression vector comprises a DNA molecule of Claim 39.

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- 42. An expression vector for expressing a Macaca mulatta AR protein wherein said expression vector comprises a DNA molecule of Claim 40.
- 43. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 41.
- 44. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 42.
  - 45. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:

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- (a) transfecting the expression vector of Claim 41 into a suitable host cell; and
- (b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said expression vector.
- 46. The process according to Claim 45 wherein the host cell is a yeast host cell.
- 47. A purified DNA molecule encoding a Macaca mulatta AR protein wherein said DNA molecule consists of the nucleotide sequence, as follows, 10 CCCAAAAAT AAAAACAAAC AAAACAAAA CAAAACAAAA AAAACGAATA AAGAAAAGG TAATAACTCA GTTCTTATTT GCACCTACTT CCAGTGGACA CTGAATTTGG AAGGTGGAGG ATTCTTGTTT TTTCTTTTAA GATCGGGCAT CTTTTGAATC TACCCCTCAA GTGTTAAGAG ACAGACTGTG AGCCTAGCAG 15 GGCAGATCTT GTCCACCGTG TGTCTTCTTT TGCAGGAGAC TTTGAGGCTG TCAGAGCGCT TTTTGCGTGG TTGCTCCCGC AAGTTTCCTT CTCTGGAGCT TCCCGCAGGT GGGCAGCTAG CTGCAGCGAC TACCGCATCA TCACAGCCTG TTGAACTCTT CTGAGCAAGA GAAGGGGAGG CGGGGTAAGG GAAGTAGGTG GAAGATTCAG CCAAGCTCAA GGATGGAGGT GCAGTTAGGG CTGGGGAGGG 20 TCTACCCTCG GCCGCCGTCC AAGACCTACC GAGGAGCTTT CCAGAATCTG TTCCAGAGCG TGCGCGAAGT GATCCAGAAC CCGGGCCCCA GGCACCCAGA GGCCGCGAGC GCAGCACCTC CCGGCGCCAG TTTGCAGCAG CAGCAGCAGC AGCAGCAAGA AACTAGCCCC CGGCAACAGC AGCAGCAGCA GCAGGGTGAG GATGGTTCTC CCCAAGCCCA TCGTAGAGGC CCCACAGGCT ACCTGGTCCT GGATGAGGAA CAGCAGCCTT CACAGCCTCA GTCAGCCCCG GAGTGCCACC 25 CCGAGAGAGG TTGCGTCCCA GAGCCTGGAG CCGCCGTGGC CGCCGGCAAG GGGCTGCCGC AGCAGCTGCC AGCACCTCCG GACGAGGATG ACTCAGCTGC CCCATCCACG TTGTCTCTGC TGGGCCCCAC TTTCCCCGGC TTAAGCAGCT GCTCCGCCGA CCTTAAAGAC ATCCTGAGCG AGGCCAGCAC CATGCAACTC CTTCAGCAAC AGCAGCAGGA AGCAGTATCC GAAGGCAGCA GCAGCGGGAG 30 AGCGAGGGAG GCCTCGGGGG CTCCCACTTC CTCCAAGGAC AATTACTTAG GGGGCACTTC GACCACTCC GACAGCGCCA AGGAGCTGTG TAAGGCAGTG TCGGTGTCCA TGGGCTTGGG TGTGGAGGCG TTGGAGCATC TGAGTCCAGG GGAACAGCTT CGGGGGGATT GCATGTACGC CCCAGTTTTG GGAGTTCCAC

|    | CCGCTGTGCG | TCCCACTCCG | TGTGCCCCAT         | TGGCCGAATG         | CAAAGGTTCT |
|----|------------|------------|--------------------|--------------------|------------|
|    | CTGCTAGACG | ACAGCGCAGG | CAAGAGCACT         | GAAGATACTG         | CTGAGTATTC |
|    | CCCTTTCAAG | GGAGGTTACA | CCAAAGGGCT         | AGAAGGCGAG         | AGCCTAGGCT |
|    | GCTCTGGCAG | CGCTGCAGCA | GGGAGCTCCG         | GGACACTTGA         | ACTGCCGTCC |
| 5  | ACCCTGTCTC | TCTACAAGTC | CGGAGCACTG         | GACGAGGCAG         | CTGCGTACCA |
|    | GAGTCGCGAC | TACTACAACT | TTCCACTGGC         | TCTGGCCGGG         | CCGCCGCCCC |
|    | CTCCACCGCC | TCCCCATCCC | CACGCTCGCA         | TCAAGCTGGA         | GAACCCGCTG |
|    | GACTATGGCA | GCGCCTGGGC | GGCTGCGGCG         | GCGCAGTGCC         | GCTATGGGGA |
|    | CCTGGCGAGC | CTGCATGGCG | CGGGTGCAGC         | GGGACCCGGC         | TCTGGGTCAC |
| 10 | CCTCAGCGGC | CGCTTCCTCA | TCCTGGCACA         | CTCTCTTCAC         | AGCCGAAGAA |
|    | GGCCAGTTGT | ATGGACCGTG | TGGTGGTGGG         | GGCGGCGGCG         | GTGGCGGCGG |
|    | CGGCGGCGGC | GCAGGCGAGG | CGGGAGCTGT         | AGCCCCTAC          | GGCTACACTC |
|    | GGCCACCTCA | GGGGCTGGCG | GGCCAGGAAG         | GCGACTTCAC         | CGCACCTGAT |
|    | GTGTGGTACC | CTGGCGGCAT | GGTGAGCAGA         | ${\tt GTGCCCTATC}$ | CCAGTCCCAC |
| 15 | TTGTGTCAAA | AGCGAGATGG | GCCCTGGAT          | GGATAGCTAC         | TCCGGACCTT |
|    | ACGGGGACAT | GCGTTTGGAG | ACTGCCAGGG         | ACCATGTTTT         | GCCAATTGAC |
|    | TATTACTTTC | CACCCCAGAA | GACCTGCCTG         | ATCTGTGGAG         | ATGAAGCTTC |
|    | TGGGTGTCAC | TATGGAGCTC | TCACATGTGG         | AAGCTGCAAG         | GTCTTCTTCA |
|    | AAAGAGCCGC | TGAAGGGAAA | CAGAAGTACC         | TGTGTGCCAG         | CAGAAATGAT |
| 20 | TGCACTATTG | ATAAATTCCG | AAGGAAAAAT         | TGTCCATCTT         | GCCGTCTTCG |
|    | GAAATGTTAT | GAAGCAGGGA | TGACTCTGGG         | AGCCCGGAAG         | CTGAAGAAAC |
|    | TTGGTAATCT | GAAACTACAG | GAGGAAGGAG         | AGGCTTCCAG         | CACCACCAGC |
|    | CCCACTGAGG | AGACAGCCCA | GAAGCTGACA         | GTGTCACACA         | TTGAAGGCTA |
|    | TGAATGTCAG | CCCATCTTTC | ${\tt TGAATGTCCT}$ | GGAGGCCATT         | GAGCCAGGTG |
| 25 | TGGTGTGTGC | TGGACATGAC | AACAACCAGC         | CCGACTCCTT         | CGCAGCCTTG |
|    | CTCTCTAGCC | TCAATGAACT | GGGAGAGAGA         | CAGCTTGTAC         | ATGTGGTCAA |
|    | GTGGGCCAAG | GCCTTGCCTG | GCTTCCGCAA         | CTTACACGTG         | GACGACCAGA |
|    | TGGCTGTCAT | TCAGTACTCC | TGGATGGGGC         | ${\tt TCATGGTGTT}$ | TGCCATGGGC |
|    | TGGCGATCCT | TCACCAATGT | CAACTCCAGG         | ATGCTCTACT         | TTGCCCCTGA |
| 30 | TCTGGTTTTC | AATGAGTACC | GCATGCACAA         | ATCCCGGATG         | TACAGCCAGT |
|    | GTGTCCGAAT | GAGGCACCTC | TCTCAAGAGT         | TTGGATGGCT         | CCAAATCACC |
|    | CCCCAGGAAT | TCCTGTGCAT | GAAAGCGCTG         | CTACTCTTCA         | GCATTATTCC |
|    | AGTGGATGGG | CTGAAAAATC | AAAAATTCTT         | TGATGAACTT         | CGAATGAACT |
|    | ACATCAAGGA | ACTCGATCGT | ATCATTGCAT         | GCAAAAGAAA         | AAATCCCACA |

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TCCTGCTCAA GGCGTTTCTA CCAGCTCACC AAGCTCCTGG ACTCCGTGCA
GCCTATTGCG AGAGAGCTGC ATCAGTTCAC TTTTGACCTG CTAATCAAGT
CACACATGGT GAGCGTGGAC TTTCCGGAAA TGATGGCAGA GATCATCTCT
GTGCAAGTGC CCAAGATCCT TTCTGGGAAA GTCAAGCCCA TCTATTTCCA
CACCCAGTGA AGCATTGGAA ATCCCTATTT CCTCACCCCA GCTCATGCCC
CCTTTCAGAT GTCTTCTGCC TGTTA, as set forth in SEQ ID NO: 3.

- 48. A DNA molecule of Claim 47 which consists of nucleotide 423 to about nucleotide 3108 of SEQ ID NO: 3.
- 49. A DNA expression vector for expressing a Macaca mulatta AR protein wherein said expression vector comprises a DNA molecule of Claim 47.
- 50. A DNA expression vector for expressing a Macaca mulatta
  AR protein wherein said expression vector comprises a DNA molecule of Claim 48.
  - 51. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 44.
- 20 52. A host cell which expresses a recombinant Macaca mulatta AR protein wherein said host cell contains the expression vector of Claim 45.
  - 53. A process for expressing a Macaca mulatta AR protein in a recombinant host cell, comprising:
- 25 (a) transfecting the expression vector of Claim 49 into a suitable host cell; and,
  - (b) culturing the host cells of step (a) under conditions which allow expression of said the Macaca mulatta AR protein from said expression vector.
- The process according to Claim 53 wherein the host cell is a yeast host cell.
  - 55. A purified Macaca mulatta AR protein which comprises the amino acid sequence as set forth in SEQ ID NO: 4.

56. A purified Macaca mulatta AR protein which consists of the amino acid sequence as set forth in SEQ ID NO: 4.

- 5 57. A purified Macaca mulatta AR protein derived from a host cell transfected with a DNA expression vector which comprises the nucleotide sequence as set forth in SEQ ID NO:3.
- 58. A purified Macaca mulatta AR protein of Claim 57 wherein said DNA expression vector contains from about nucleotide 423 to about nucleotide 3108 of SEQ ID NO:3.

| 1    | CCCAAAAAAT  | AAAAACAAAC | AAAAACAAAA | CAAAACAAAA | AAAACGAATA |
|------|-------------|------------|------------|------------|------------|
| 51   | AAGAAAAAGG  | TAATAACTCA | GTTCTTATTT | GCACCTACTT | CCAGTGGACA |
| 101  | CTGAATTTGG  | AAGGTGGAGG | ATTCTTGTTT | TITCTTTTAA | GATCGGGCAT |
| 151  | CTTTTGAATC  | TACCCCTCAA | GTGTTAAGAG | ACAGACTGTG | AGCCTAGCAG |
| 201  | GGCAGATCTT  | GTCCACCGTG | TGTCTTCTTT | TGCAGGAGAC | TTTGAGGCTG |
| 251  | TCAGAGCGCT  | TTTTGCGTGG | TTGCTCCCGC | AAGTTTCCTT | CTCTGGAGCT |
| 301  | TCCCGCAGGT  | GGGCAGCTAG | CTGCAGCGAC | TACCGCATCA | TCACAGCCTG |
| 351  | TTGAACTCTT  | CTGAGCAAGA | GAAGGGGAGG | CGGGGTAAGG | GAAGTAGGTG |
| 401  | GAAGATTCAG  | CCAAGCTCAA | GGATGGAGGT | GCAGTTAGGG | CTGGGGAGGG |
| 451  | TCTACCCTCG  | GCCGCCGTCC | AAGACCTACC | GAGGAGCTTT | CCAGAATCTG |
| 501  | TTCCAGAGCG  | TGCGCGAAGT | GATCCAGAAC | CCGGGCCCCA | GGCACCCAGA |
| 551  | GGCCGCGAGC  | GCAGCACCTC | CCGGCGCCAG | TTTGCAGCAG | CAGCAGCAGC |
| 601  | AGCAGCAAGA  | AACTAGCCCC | CGGCAACAGC | AGCAGCAGCA | GCAGGGTGAG |
| 651  | GATGGTTCTC  | CCCAAGCCCA | TCGTAGAGGC | CCCACAGGCT | ACCTGGTCCT |
| 701  | GGATGAGGAA  | CAGCAGCCTT | CACAGCCTCA | GTCAGCCCCG | GAGTGCCACC |
| 751  | CCGAGAGAGG  | TTGCGTCCCA | GAGCCTGGAG | CCGCCGTGGC | CGCCGGCAAG |
| 801  | GGGCTGCCGC  | AGCAGCTGCC | AGCACCTCCG | GACGAGGATG | ACTCAGCTGC |
| 851  | CCCATCCACG  | TTGTCTCTGC | TGGGCCCCAC | TTTCCCCGGC | TTAAGCAGCT |
| 901  | GCTCCGCCGA  | CCTTAAAGAC | ATCCTGAGCG | AGGCCAGCAC | CATGCAACTC |
| 951  | CTTCAGCAAC  | AGCAGCAGGA | AGCAGTATCC | GAAGGCAGCA | GCAGCGGGAG |
| 1001 | AGCGAGGGAG  | GCCTCGGGGG | CTCCCACTTC | CTCCAAGGAC | AATTACTTAG |
| 1051 | _AGGGCACTTC | GACCATTTCT | GACAGCGCCA | AGGAGCTGTG | TAAGGCAGTG |
| 1101 | TCGGTGTCCA  | TGGGCTTGGG | TGTGGAGGCG | TTGGAGCATC | TGAGTCCAGG |
| 1151 | GGAACAGCTT  | CGGGGGGATT | GCATGTACGC | CCCAGTTTTG | GGAGTTCCAC |
| 1201 | CCGCTGTGCG  | TCCCACTCCG | TGTGCCCCAT | TGGCCGAATG | CAAAGGTTCT |

FIG.1A

| 1251 | CTGCTAGACG | ACAGCGCAGG | CAAGAGCACT | GAAGATACTG | CTGAGTATTC |
|------|------------|------------|------------|------------|------------|
| 1301 | CCCTTTCAAG | GGAGGTTACA | CCAAAGGGCT | AGAAGGCGAG | AGCCTAGGCT |
| 1351 | GCTCTGGCAG | CGCTGCAGCA | GGGAGCTCCG | GGACACTTGA | ACTGCCGTCC |
| 1401 | ACCCTGTCTC | TCTACAAGTC | CGGAGCACTG | GACGAGGCAG | CTGCGTACCA |
| 1451 | GAGTCGCGAC | TACTACAACT | TTCCACTGGC | TCTGGCCGGG | CCGCCGCCCC |
| 1501 | CTCCACCGCC | TCCCCATCCC | CACGCTCGCA | TÇAAGCTGGA | GAACCCGCTG |
| 1551 | GACTATGGCA | GCGCCTGGGC | GGCTGCGGCG | GCGCAGTGCC | GCTATGGGGA |
| 1601 | CCTGGCGAGC | CTGCATGGCG | CGGGTGCAGC | GGGACCCGGC | TCTGGGTCAC |
| 1651 | CCTCAGCGGC | CGCTTCCTCA | TCCTGGCACA | CTCTCTTCAC | AGCCGAAGAA |
| 1701 | GGCCAGTTGT | ATGGACCGTG | TGGTGGTGGG | GGCGGCGGCG | GTGGCGGCGG |
| 1751 | CGGCGGCGGC | GCAGGCGAGG | CGGGAGCTGT | AGCCCCCTAC | GGCTACACTC |
| 1801 | GGCCACCTCA | GGGGCTGGCG | GGCCAGGAAG | GCGACTTCAC | CGCACCTGAT |
| 1851 | GTGTGGTACC | CTGGCGGCAT | GGTGAGCAGA | GTGCCCTATC | CCAGTCCCAC |
| 1901 | TTGTGTCAAA | AGCGAGATGG | GCCCCTGGAT | GGATAGCTAC | TCCGGACCTT |
| 1951 | ACGGGGACAT | GCGTTTGGAG | ACTGCCAGGG | ACCATGTTTT | GCCAATTGAC |
| 2001 | TATTACTTTC | CACCCCAGAA | GACCTGCCTG | ATCTGTGGAG | ATGAAGCTTC |
| 2051 | TGGGTGTCAC | TATGGAGCTC | TCACATGTGG | AAGCTGCAAG | GTCTTCTTCA |
| 2101 | AAAGAGCCGC | TGAAGGGAAA | CAGAAGTACC | TGTGTGCCAG | CAGAAATGAT |
| 2151 | TGCACTATTG | ATAAATTCCG | AAGGAAAAAT | TGTCCATCTT | GCCGTCTTCG |
| 2201 | GAAATGTTAT | GAAGCAGGGA | TGACTCTGGG | AGCCCGGAAG | CTGAAGAAAC |
| 2251 | TTGGTAATCT | GAAACTACAG | GAGGAAGGAG | AGGCTTCCAG | CACCACCAGC |
| 2301 | CCCACTGAGG | AGACAGCCCA | GAAGCTGACA | GTGTCACACA | TTGAAGGCTA |
| 2351 | TGAATGTCAG | CCCATCTTTC | TGAATGTCCT | GGAGGCCATT | GAGCCAGGTG |
| 2401 | TGGTGTGTGC | TGGACATGAC | AACAACCAGC | CCGACTCCTT | CGCAGCCTTG |
| 2451 | CTCTCTAGCC | TCAATGAACT | GGGAGAGAGA | CAGCTTGTAC | ATGTGGTCAA |

FIG.1B

| 2501 | GTGGGCCAAG | GCCTTGCCTG  | GCTTCCGCAA | CTTACACGTG | GACGACCAGA |
|------|------------|-------------|------------|------------|------------|
| 2551 | TGGCTGTCAT | TCAGTACTCC  | TGGATGGGGC | TCATGGTGTT | TGCCATGGGC |
| 2601 | TGGCGATCCT | TCACCAATGT  | CAACTCCAGG | ATGCTCTACT | TTGCCCCTGA |
| 2651 | TCTGGTTTTC | AATGAGTACC  | GCATGCACAA | ATCCCGGATG | TACAGCCAGT |
| 2701 | GTGTCCGAAT | GAGGCACCTC  | TCTCAAGAGT | TTGGATGGCT | CCAAATCACC |
| 2751 | CCCCAGGAAT | TCCTGTGCAT  | GAAAGCGCTG | CTACTCTTCA | GCATTATTCC |
| 2801 | AGTGGATGGG | CTGAAAAATC  | AAAAATTCTT | TGATGAACTT | CGAATGAACT |
| 2851 | ACATCAAGGA | ACTCGATCGT  | ATCATTGCAT | GCAAAAGAAA | AAATCCCACA |
| 2901 | TCCTGCTCAA | GGCGTTTCTA  | CCAGCTCACC | AAGCTCCTGG | ACTCCGTGCA |
| 2951 | GCCTATTGCG | AGAGAGCTGC  | ATCAGTTCAC | TTTTGACCTG | CTAATCAAGT |
| 3001 | CACACATGGT | GAGCGTGGAC  | TTTCCGGAAA | TGATGGCAGA | GATCATCTCT |
| 3051 | GTGCAAGTGC | CCA'AGATCCT | TTCTGGGAAA | GTCAAGCCCA | TCTATTTCCA |
| 3101 | CACCCAGTGA | AGCATTGGAA  | ATCCCTATTT | CCTCACCCCA | GCTCATGCCC |
| 3151 | CCTTTCAGAT | GTCTTCTGCC  | TGTTA (SEQ | ID NO:1)   |            |

FIG.1C

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1 MEVOLGLGRV YPRPPSKTYR GAFONLFOSV REVIONPGPR HPEAASAAPP 51 GASLOOOOO OOETSPROOO OOOOGEDGSP OAHRRGPTGY LVLDEEQQPS 101 QPQSAPECHP ERGCVPEPGA AVAAGKGLPQ QLPAPPDEDD SAAPSTLSLL 151 GPTFPGLSSC SADLKDILSE ASTMQLLQQQ QQEAVSEGSS SGRAREASGA 201 PTSSKDNYLE GTSTISDSAK ELCKAVSVSM GLGVEALEHL SPGEQLRGDC 251 MYAPVLGVPP AVRPTPCAPL AECKGSLLDD SAGKSTEDTA EYSPFKGGYT 301 KGLEGESLGC SGSAAAGSSG TLELPSTLSL YKSGALDEAA AYQSRDYYNF 351 PLALAGPPPP PPPPHPHARI KLENPLDYGS AWAAAAAQCR YGDLASLHGA 401 GAAGPGSGSP SAAASSSWHT LFTAEEGQLY GPCGGGGGGG GGGGGGAGEA 451 GAVAPYGYTR PPQGLAGQEG DFTAPDVWYP GGMVSRVPYP SPTCVKSEMG 501 PWMDSYSGPY GDMRLETARD HVLPIDYYFP PQKTCLICGD EASGCHYGAL 551 TCGSCKVFFK RAAEGKQKYL CASRNDCTID KFRRKNCPSC RLRKCYEAGM 601 TLGARKLKKL GNLKLQEEGE ASSTTSPTEE TAQKLTVSHI EGYECQPIFL 651 NVLEAIEPGV VCAGHDNNQP DSFAALLSSL NELGERQLVH VVKWAKALPG 701 FRNLHVDDQM AVIQYSWMGL MVFAMGWRSF TNVNSRMLYF APDLVFNEYR 751 MHKSRMYSOC VRMRHLSOEF GWLQITPQEF LCMKALLLFS IIPVDGLKNQ 801 KFFDELRMNY IKELDRIIAC KRKNPTSCSR RFYQLTKLLD SVQPIARELH 851 OFTFDLLIKS HMVSVDFPEM MAEIISVQVP KILSGKVKPI YFHTQ (SEQ ID NO:2)

FIG.2

| 1            | CCCAAAAATAAAAACAAACAAAACAAAACAAAACAAAAAA  | 60   |
|--------------|---|------|
| T            | GGGTTTTTATTTTGTTTGTTTTGTTTTGTTTTTGTTTTTCC   | 00   |
| 61           | TAATAACTCAGTTCTTATTTGCACCTACTTCCAGTGGACACTGAATTTGGAAGGTGGAGG  | 120  |
| 01           | ATTATTGAGTCAAGAATAAACGTGGCTGAAGGTCACCTGTGACTTAAACCTTCCACCTCC  | 120  |
| 121          | ATTCTTGTTTTTTTTTAAGATCGGGCATCTTTTGAATCTACCCCTCAAGTGTTAAGAG  | 180  |
| 121          | TAAGAACAAAAAAGAAAATTCTAGCCCGTAGAAAACTTAGATGGGGAGTTCACAATTCTC  | 100  |
| 181          | ACAGACTGTGAGCCTAGCAGGGCAGATCTTGTCCACCGTGTGTCTTCTTTTGCAGGAGAC  | 240  |
| 101          | TGTCTGACACTCGGATCGTCCCGTCTAGAACAGGTGGCACACAGAAGAAAACGTCCTCTG  | 240  |
| 241          | TTTGAGGCTGTCAGAGCGCTTTTTGCGTGGTTGCTCCCGCAAGTTTCCTTCTCTGGAGCT  | 300  |
| Z41          | AAACTCCGACAGTCTCGCGAAAAACGCACCAACGAGGGCGTTCAAAGGAAGAGACCTCGA  | 500  |
| 301          | TCCCGCAGGTGGGCAGCTAGCTGCAGCGACTACCGCATCATCACAGCCTGTTGAACTCTT  | 360  |
| 301          | AGGGCGTCCACCCGTCGATCGACGTCGCTGATGGCGTAGTAGTGTCGGACAACTTGAGAA  | 500  |
| 361          | CTGAGCAAGAGAAGGGGAGGCGGGGTAAGGGAAGTAGGTGGAAGATTCAGCCAAGCTCAA  | 420  |
| 301          | GACTCGTTCTCTCCCCTCCGCCCCATTCCCTTCATCCACCTTCTAAGTCGGTTCGAGTT   | 420  |
| 421          | GGATGGAGGTGCAGTTAGGGCTGGGGAGGGTCTACCCTCGGCCGCCGTCCAAGACCTACC  | 480  |
| 721          | CCTACCTCCACGTCAATCCCGACCCCTCCCAGATGGGAGCCGGCGGCAGGTTCTGGATGG<br>M E V Q L G L G R V Y P R P P S K T Y R | 480  |
|              | GAGGAGCTTTCCAGAATCTGTTCCAGAGCGTGCGCGAAGTGATCCAGAACCCGGGCCCCA  | 540  |
| 481          | CTCCTCGAAAGGTCTTAGACAAGGTCTCGCACGCGCTTCACTAGGTCTTGGGCCCGGGGT<br>G A F Q N L F Q S V R E V I Q N P G P R | .540 |
| <i>C 1</i> 1 | GGCACCCAGAGGCCGCGAGCGCAGCACCTCCCGGCGCCAGTTTGCAGCAGCAGCAGCAGC  | 600  |
| 541          | CCGTGGGTCTCCGGCGCTCGTCGTGGAGGGCCGCGGTCAAACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC                       | 000  |
| C01          | AGCAGCAAGAAACTAGCCCCCGGCAACAGCAGCAGCAGCAGCAGGGTGAGGATGGTTCTC  | 660  |
| 601          | TCGTCGTTCTTTGATCGGGGGCCGTTGTCGTCGTCGTCGTCGTCCCACTCCTACCAAGAG<br>Q Q E T S P R Q Q Q Q Q Q G E D G S P   | 000  |
| 661          | CCCAAGCCCATCGTAGAGGCCCCACAGGCTACCTGGTCCTGGATGAGGAACAGCAGCCTT  | 720  |
| OOT          |   |      |

FIG.3A

|      | Q A H R R G P T G Y L V L D E E Q Q P S  |      |
|------|--|------|
| 721  | CACAGCCTCAGTCAGCCCCGGAGTGCCACCCCGAGAGAGGTTGCGTCCCAGAGCCTGGAG GTGTCGGAGTCAGTCGGGGCCTCACGGTGGGGCTCTCTCCAACGCAGGGTCTCGGACCTC Q P Q S A P E C H P E R G C V P E P G A    | 780  |
| 781  | CCGCCGTGGCCGCCAAGGGGCTGCCGCAGCAGCTGCCAGCACCTCCGGACGAGGATG GGCGGCACCGGCGCGTTCCCCGACGGCGTCGTCGACGGTCGTGGAGGCCTGCTCCTAC A V A A G K G L P Q Q L P A P P D E D D         | 840  |
| 841  | ACTCAGCTGCCCCATCCACGTTGTCTCTGCTGGGCCCCACTTTCCCCGGCTTAAGCAGCT TGAGTCGACGGGGTAGGTGCAACAGAGACGACCCGGGGTGAAAGGGGCCGAATTCGTCGA S A A P S T L S L L G P T F P G L S S C    | 900  |
| 901  | GCTCCGCCGACCTTAAAGACATCCTGAGCGAGGCCAGCACCATGCAACTCCTTCAGCAAC CGAGGCGGCTGGAATTTCTGTAGGACTCGCTCCGGTCGTGGTACGTTGAGGAAGTCGTTG S A D L K D I L S E A S T M Q L L Q Q Q    | 960  |
| 961  | AGCAGCAGGAAGCAGTATCCGAAGGCAGCAGCAGCGGGAGAGCGAGGGAGG  | 1020 |
| 1021 | CTCCCACTTCCTCCAAGGACAATTACTTAGAGGGCACTTCGACCATTTCTGACAGCGCCA GAGGGTGAAGGAGGTTCCTGTTAATGAATCTCCCGTGAAGCTGGTAAAGACTGTCGCGGT P T S S K D N Y L E G T S T I S D S A K    | 1080 |
| 1081 | AGGAGCTGTGTAAGGCAGTGTCGGTGTCCATGGGCTTGGGTGTGGAGCGTTGGAGCATC  TCCTCGACACATTCCGTCACAGCCACAGGTACCCGAACCCTCCGCAACCTCGTAG  E L C K A V S V S M G L G V E A L E H L        | 1140 |
| 1141 | TGAGTCCAGGGGAACAGCTTCGGGGGGGATTGCATGTACGCCCCAGTTTTGGGAGTTCCAC  ACTCAGGTCCCCTTGTCGAAGCCCCCCTAACGTACATGCGGGGTCAAAACCCTCAAGGTG  S P G E Q L R G D C M Y A P V L G V P P | 1200 |
| 1201 | CCGCTGTGCGTCCCACTCCGTGTGCCCCATTGGCCGAATGCAAAGGTTCTCTGCTAGACG GGCGACACGCAGGGTGAGGCACACGGGGTAACCGGCTTACGTTTCCAAGAGACGATCTGC A V R P T P C A P L A E C K G S L L D D    | 1260 |
| 1261 | ACAGCGCAGGCAAGAGCACTGAAGATACTGCTGAGTATTCCCCTTTCAAGGGAGGTTACA   | 1320 |

FIG.3B

|       | TGTC      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | ATG<br>Y  |   |       |
|-------|-----------|------------------|----------|----------|-----------|-----------|-----------|-----------------------|-----------|-----------|------------------|-----------|------|--------------|-----------|-----------------------|-----------|-----------|-----------|---|-------|
| 1321  | CCAA      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           |           |   | 1380  |
| 1021  | GGTT<br>K | TCC<br>G         | CGA<br>L | TCT<br>E | TCC(<br>G | GCT(<br>E | CTC(<br>S | GGA <sup>-</sup><br>L | TCC(<br>G | GAC(<br>C | GAG/<br>S        | ACC(<br>G | STC( | GCG/<br>A    | ACGT<br>A | rcg <sup>-</sup><br>A | TCC(<br>G | CTC(<br>S | GAGG<br>S | С | 1000  |
| 1381  | GGAC      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           |           |   | 1440  |
| 1001  | CCTG      | TGA              | ACT      | TGA      | CGG       |           | GTG(      | GGA                   | CAGA      | AGA(      | GAT(             | STT(      | CAG  | GCCT         | CG        | ΓGA(                  | CCT       |           |           |   | 1770  |
| 1441  | CTGC      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           |           |   | 1500  |
| 1771  | GACG      | CAT              | GGT      | СТС      | AGC       | GCT(      | GAT       | GAT(                  | GTT(      | AAE       | AGG <sup>-</sup> | TGA       | CCGA | AGA(         | CGC       | GCC                   | CGG       | CGG       |           | G | 1000  |
| 1501  | CTCC      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | ГGGC<br>  |   | 1560  |
|       | GAGG<br>P |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | ACCG<br>G |   |       |
| 1561  | GCGC      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | rggc      |   | 1620  |
| 2001  | CGCG<br>A |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | ACCG<br>G | С |       |
| 1621  | CGGG      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | GCAC      |   | 1680  |
| 1021  | GCCC      | ACG <sup>*</sup> | TCG      | CCC      | TGG       |           | GAG/      | ACC(                  | CAG       | TGG(      | GAG              | rcg(      | CCG  | GCG/         | \AG(      | GAG                   | TAG(      | GAC(      |           |   | 1000  |
| 1681  | CTCT      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | CGGC      |   | 1740  |
| 1001  | GAGA      | GAA              | GTG      | TCG      | GCT       | TCT       | TCC       | GGT(                  | CAA(      | CATA      | ACC.             | TGG(      | CACA | ACC <i>A</i> | ACC/      | ACC(                  | CCC       | GCC(      |           | С | 17.10 |
| 1741  | GTGG      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           | CACT      |   | 1800  |
| 1, 11 | CACC      | GCC              | GCC      | GGC      | GCC       | GCC       | GCG       | TCC(                  | GCT(      | CCG       | CCC              | rcg/      | ACA7 | rcge         | GGG       | GAT(                  | GCC(      | GATO      |           | G |       |
| 1801  | GGCC      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           |           |   | 1860  |
| 1001  | CCGG      | TGG              | AGT      | CCC      | CGA       | CCG       | CCC       | GGT(                  | CCT       | TCC(      | GCT(             | SAA(      | GTG  | GCG1         | rgg/      | ACT/                  | ACA(      | CAC       |           | G | 1000  |
| 1861  | CTGG      |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           |           |   | 1920  |
|       |           |                  |          |          |           |           |           |                       |           |           |                  |           |      |              |           |                       |           |           |           |   |       |

|      | GACCGCCGTACCACTCGTCTCACGGGATAGGGTCAGGGTGAACACAGTTTTCGCTCTACC G G M V S R V P Y P S P T C V K S E M G                        |      |
|------|---|------|
| 1921 | GCCCCTGGATGGATAGCTACTCCGGACCTTACGGGGACATGCGTTTGGAGACTGCCAGGG  | 1980 |
|      | CGGGGACCTACCTATCGATGAGGCCTGGAATGCCCCTGTACGCAAACCTCTGACGGTCCC PWMDSYSGPYGDMRLETARD   |      |
| 1981 | ACCATGTTTTGCCAATTGACTATTACTTTCCACCCCAGAAGACCTGCCTG  | 2040 |
|      | H V L P I D Y Y F P P Q K T <u>C L I C G D</u>  |      |
| 2041 | ATGAAGCTTCTGGGTGTCACTATGGAGCTCTCACATGTGGAAGCTGCAAGGTCTTCTTCA+ TACTTCGAAGACCCACAGTGATACCTCGAGAGTGTACACCTTCGACGTTCCAGAAGAAGT  | 2100 |
|      | EASGCHYGALTCGSCKVFFK  |      |
| 2101 | AAAGAGCCGCTGAAGGGAAACAGAAGTACCTGTGTGCCAGCAGAAATGATTGCACTATTG++ TTTCTCGGCGACTTCCCTTTGTCTTCATGGACACACGGTCGTCTTTACTAACGTGATAAC | 2160 |
|      | RAAEGKQKYLCASRNDCTID  |      |
| 2161 | ATAAATTCCGAAGGAAAAATTGTCCATCTTGCCGTCTTCGGAAATGTTATGAAGCAGGGA+ TATTTAAGGCTTCCTTTTTAACAGGTAGAACGGCAGAAGCCTTTACAATACTTCGTCCCT  | 2220 |
|      | KFRRKNCPSCRLRKCYEAGM  |      |
| 2221 | TGACTCTGGGAGCCCGGAAGCTGAAGAAACTTGGTAATCTGAAACTACAGGAGGAAGGA   | 2280 |
|      | T L G A R K L K K L G N L K L Q E E G E AGGCTTCCAGCACCACCAGCCCCACTGAGGAGACAGCCCAGAAGCTGACAGTGTCACACA                        |      |
| 2281 | TCCGAAGGTCGTGGTCGGGGTGACTCCTCTGTCGGGTCTTCGACTGTCACAGTGTGT   | 2340 |
|      | A S S T T S P T E E T A Q K L T V S H I  TTGAAGGCTATGAATGTCAGCCCATCTTTCTGAATGTCCTGGAGGCCATTGAGCCAGGTG                       |      |
| 2341 | AACTTCCGATACTTACAGTCGGGTAGAAAGACTTACAGGACCTCCGGTAACTCGGTCCAC  | 2400 |
|      | E G Y E C Q P I F L N V L E A I E P G V TGGTGTGTGCTGGACATGACAACAACCAGCCCGACTCCTTCGCAGCCTTGCTCTCTAGCC                        |      |
| 2401 | ACCACACGACCTGTACTGTTGTTGGTCGGGCTGAGGAAGCGTCGGAACGAGAGATCGG  | 2460 |
|      | V C A G H D N N Q P D S F A A L L S S L TCAATGAACTGGGAGAGAGACAGCTTGTACATGTGGTCAAGTGGGCCAAGGCCTTGCCTG                        |      |
| 2461 |   | 2520 |

| AGTT<br>N | ACT<br>E   | TGA<br>L  | CCC <sup>-</sup><br>G  | TCT(<br>E  | CTC <sup>*</sup><br>R  | TGT(<br>Q   | CGA/<br>L   | ACA <sup>-</sup><br>V   | ГGT/<br>Н  | ACA(<br>V  | CCA(<br>V  | GTT(<br>K   | CAC(<br>W   | CCG(<br>A  | GTT(<br>K   | CCG(<br>A   | GAA(<br>L   | CGGAC<br>P G   |  |
|-----------|--|---|--|--|--|---|---|---|--|--|--|---|---|--|---|---|---|--|--|
| GCTT      | CCG  | CAA(  | CTT  | 4CA(   |  |   |   |   |  |  |  |   |   |  |   |   | GAT(  | GGGGC  | 2580   |
| CGAA<br>F | GGC(<br>R  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 2000   |
|           |  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 2640   |
| AGTA      | CCA  | CAA   | ACG(   | GTA  | CCC  | GAC(  | CGC   | TAG(  | GAA(   | GTG(   | TTE  | 4CA   | GTT(  | GAG  | GTC   | CTA   |   |  |  |
| TTGC      | CCC  | TGA   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 2700   |
|           |  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  |  |
| GTGT      | CCG.   | AAT(<br>+   | GAG(   | GCA  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 2760   |
|           |  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  |  |
| TCCT      |  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 2820   |
|           |  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  |  |
| AAAA      | ATT  | CTT   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 2880   |
|           |  |   | ACT  | ACT  | TGA  | AGC <sup>*</sup>  | TTA   | CTT   | GATO   | STA(   | GTT(   | CCT   | TGA   | GCT.   | AGC.  | ATA   | GTA   |  | 2000   |
|           |  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 2940   |
| CGTT      | TTC  | ПТ  | TTT  | AGG  | GTG  | TAG   | GAC   | GAG   | TTC  | CGC/   | 444  | GAT   | GGT   | CGA  | GTG   | GTT   | CGA   | GGACC  |  |
|           |  |   |  |  |  |   |   |   |  |  |  |   |   |  |   |   |   |  | 3000   |
| TGAG      | <b>GCA</b>   | CGT   | CGG  | ATA  | ACG  | CTC   | TCT   | CGA   | CGTA   | AGT(   | CAA  | GTG   | AAA   | ACT  | GGA   | CGA   | TTA   | GTTCA  |  |
| CACA      | CAT  | GGT   | GAG  | CGT  | GGA  | CTT<br>+  | TCC   | GGA   | AAT(<br>-+-  | GAT(   | GGC.   | AGA   | GAT   | CAT  | CTC   | TGT<br>+  | GCA   | AGTGC  | 3060   |
| GTGT      | GTA  | CCA   | CTC  | GCA  | CCT  | GAA   | AGG   | CCT   | TTA  | CTA  | CCG  | TCT   | CTA   | GTA  | GAG   | ACA   | CGT   | TCACG  |  |
| CCAA      | GAT  | CCT   | TTC  | TGG  | GAA  | AGT<br>+  | CAA   | GCC   | CAT(   | CTA <sup>-</sup>   | TTT  | CCA<br>+  | CAC   | CCA  | GTG   | AAG<br>+  | CAT   | TGGAA  | 3120   |
|           | CGAA  TTGC  AACG  ACG  ACG | GCTTCCGCCAAGGCAACAGATCCCAAGATCCCAAGATCCCAAGAGCAGAGCAGAGCAGAGCAGAGGCAAGAGGCAACAGAGGCAACAGAGGCAACAGAGGCAACAGAGATCCCAAGAGATCCGAAGAGCAACAGAGAGCAACAGAGAGCAACAGAGAGCAACAGAGAGCAACAGAGAGCAACAGAGAGAGCAACACACACACAGAGAGAGCAACAGAGAGAGCAACAGAGAGAGCAACAGAGAGAGAGAGAGAGAGAGCAACAG | GCTTCCGCAAG CGAAGGCGTTG FRN  TCATGGTGTT AGTACCACAAA MVF  TTGCCCCTGAA AACGGGGACTAA A P D  GTGTCCGAATA VRM  TCCTGTGCATA VRM  TCCTGTGCATA L C M  AAAAATTCTT ATTTTAAGAAA KFF  GCAAAAGAAAA CGTTTTCTTT KRK  ACTCCGTGCA TGAGGCACGTA L C M  CGTTTTCTTT KRK  ACTCCGTGCA TGAGGCACGTA CGTTTTCTTT KRK  CGTTTTCTTT  CGTTTTCTT  CGTTTTCTT  CGTTTTCTT  CGTTTTCTT  CGTTTT  CGTTTTCTT  CGTTTT  CGTTTT  CGTTTT  CGTTTT  CGTTTT  CGTTTT  CGTTT  CGTTT  CGTTT  CGTTT  CGTTT  CGTTT  CGTTT  CGTTT  CGTT  CGTT | GCTTCCGCAACTTA CGAAGGCGTTGAA FRNL  TCATGGTGTTTGCC AGTACCACAAACGC MVFA  TTGCCCCTGATCTC AACGGGGACTAGAC APDL  GTGTCCGAATGAGC CACAGGCTTACTC VRMR  TCCTGTGCATGAAAAAAAAAAAAAAAAAAAAAAAATTCTTTGAAAAAAATTCTTTGAAAAAAAA | GCTTCCGCAACTTACAACTACAACGAAGGCGTTGAATGTC FRNLH TCATGGTGTTTGCCATCACACACACACACACACACGGTACTACTCGGT AACGGGGACTACTACTCCGTCACACACACACACACACACA | N E L G E R  GCTTCCGCAACTTACACGTO CGAAGGCGTTGAATGTGCAO F R N L H V  TCATGGTGTTTGCCATGGG AGTACCACAAACGGTACCCO M V F A M G  TTGCCCCTGATCTGGTTTTO AACGGGGACTAGACCAAAA A P D L V F  GTGTCCGAATGAGGCACCT CACAGGCTTACTCCGTGGAO V R M R H L  TCCTGTGCATGAAAGCGCTO AGGACACGTACTTTCGCGAO L C M K A L  AAAAATTCTTTGATGAACT TTTTTAAGAAACTACTTGAO K F F D E L  GCAAAAGAAAAAATCCCAC CGTTTTCTTTTTTTAGGGTG K R K N P T  ACTCCGTGCAGCCTATTGC TGAGGCACGTCGGATAACG S V Q P I A  CACACATGGTGAGCGTGGAA  CACACATGGTGAGCGTGGAA  CACACATGGTGAGCGTGGAA  CACACATGGTGAGCGTGGAA  CTGTGTACCACTCGCACCT H M V S V D  CCCAAGATCCTTTCTGGGAAA  CCCAAGATCCTTTCTGGGAAA  CCCAAGATCCTTTCTGGGAAA  CCCAAGATCCTTTCTGGGAAA  CCCAAGATCCTTTCTGGGAAA  CCCAAGATCCTTTCTGGGAAA | GCTTCCGCAACTTACACGTGGAGCACTTACACGTGGAGCAGAGGCGTTGAATGTGCACCTGFR N L H V D  TCATGGTGTTTGCCATGGGCTGGAGAGTACCACAAACGGTACCCGACGACAAACGGTACCCGACGACAAACGGTACCCGACGACAAACGGTACCCGACGACAAACGTTACAAAAAAAA | N E L G E R Q L  GCTTCCGCAACTTACACGTGGACGAC CGAAGGCGTTGAATGTGCACCTGCTC F R N L H V D D  TCATGGTGTTTGCCATGGGCTGGCGC AGTACCACAAACGGTACCCGACCGC M V F A M G W R  TTGCCCCTGATCTGGTTTTCAATGAC AACGGGGACTAGACCACAAAAGTTACTC A P D L V F N E  GTGTCCGAATGAGGCACCTCTCTCAC CACAGGCTTACTCCGTGGAGAGAGT V R M R H L S Q  TCCTGTGCATGAAAGCGCTGCTACTC AGGACACGTACTTTCGCGACGATGAC L C M K A L L L  AAAAATTCTTTGATGAACTTCGAATC K F F D E L R M  GCAAAAGAAAAAATCCCACATCCTGC K R K N P T S C  ACTCCGTGCAGCAGCTTACTCGCACTCTCTC S V Q P I A R E  CACACATGGTGAGCCTCCACACCTCCTCCACACCCTCCTCCACCCCCACCTCCT | N E L G E R Q L V  GCTTCCGCAACTTACACGTGGACGACCAC CGAAGGCGTTGAATGTGCACCTGCTGGTG F R N L H V D D Q  TCATGGTGTTTGCCATGGGCTGGCGATCC AGTACCACAAACGGTACCCGACCGCTAGC M V F A M G W R S  TTGCCCCTGATCTGGTTTTCAATGAGTAC A P D L V F N E Y  GTGTCCGAATGAGGCACCTCTCTCAAGAC CACAGGCTTACTCCGTGGAGAGAGAGTCTC V R M R H L S Q E  TCCTGTGCATGAAAGCGCTGCTACTCTTC AGGACACGTACTTTCGCGACGATGAGAAC L C M K A L L F  AAAAATTCTTTGATGAACTTCGAATGAAC TTTTTAAGAAAACTACTTGAAGCTTACTTC K F F D E L R M N  GCAAAAGAAAAAAATCCCACATCCTGCTC CGTTTTCTTTTTTAGGGTGTAGGACGAG K R K N P T S C S  ACTCCGTGCAGCCTGATACGCTCTCTCCGAA S V Q P I A R E L  CACACATGGTGAGCCTCCTCTCCGAA GTGTGTACCACTCTGCAACGCCTCTCTCCGAA GTGTGTACCACTCTGCAACGCCTCTCTCCGAA GTGTGTACCACTCGGACCATCCTGCTC H M V S V D F P E  CCAAGATCCTTTCTGGGAAAGGCCTT | N E L G E R Q L V H  GCTTCCGCAACTTACACGTGGACGACCAGATC  CGAAGGCGTTGAATGTGCACCTGCTGGTCTAC F R N L H V D D Q M  TCATGGTGTTTGCCATGGGCTGGCGATCCTTC  AGTACCACAAACGGTACCCGACCGCTAGGAAC M V F A M G W R S F  TTGCCCCTGATCTGGTTTTCAATGAGTACCGC A P D L V F N E Y R  GTGTCCGAATGAGGCACCTCTCTCAAGAGTT  CACAGGCTTACTCCGTGGAGAGAGTTCTCAAC V R M R H L S Q E F  TCCTGTGCATGAAAGCGCTGCTACTCTTCAGC L C M K A L L L F S  AAAAATTCTTTGATGAACTTCGAATGAACTAC K F F D E L R M N Y  GCAAAAGAAAAAAAACTACTTGAAGCTTACTTGATC K F F D E L R M N Y  GCAAAAGAAAAAAAACCCACATCCTGCTCAAGC  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FIG.3E

10/10

FIG.3F

### SEQUENCE LISTING

<110> Merck & Co., Inc.

<130> 20736 PCT

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Ser Pro Arg Gln Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro 65 70 75 . 80

Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu
85 90 95

Gln Gln Pro Ser Gln Pro Gln Ser Ala Pro Glu Cys His Pro Glu Arg

100 105 110

Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Gly Lys Gly Leu
115 120 125

Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro 130 135 140

Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys 145 150 155 160

Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu
165 170 175

| Leu | Gln | Gln | Gln | Gln | Gln | Glu | Ala | Val | Ser | Glu | Gly | Ser | Ser | Ser | Gly |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ala | Arg | Glu | Ala | Ser | Gly | Ala | Pro | Thr | Ser | Ser | Lys | Asp | Asn | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Glu | Gly | Thr | Ser | Thr | Ile | Ser | Asp | Ser | Ala | Lys | Glu | Leu | Cys | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Val | Ser | Val | Ser | Met | Gly | Leu | Gly | Val | Glu | Ala | Leu | Glu | His | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Pro | Gly | Glu | Gln | Leu | Arg | Gly | Asp | Cys | Met | Tyr | Ala | Pro | Val | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Val | Pro | Pro | Ala | Val | Arg | Pro | Thr | Pro | Cys | Ala | Pro | Leu | Ala | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Cys | Lys | Gly | Ser | Leu | Leu | Asp | Asp | Ser | Ala | Gly | Lys | Ser | Thr | Glu | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Ala | Glu | Tyr | Ser | Pro | Phe | Lys | Gly | Gly | Tyr | Thr | Lys | Gly | Leu | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Glu | Ser | Leu | Gly | Cys | Ser | Gly | Ser | Ala | Ala | Ala | Gly | Ser | Ser | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Leu | Glu | Leu | Pro | Ser | Thr | Leu | Ser | Leu | Tyr | Lys | Ser | Gly | Ala | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Glu | Ala | Ala | Ala | Tyr | Gln | Ser | Arg | Asp | Tyr | Tyr | Asn | Phe | Pro | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Leu | Ala | Gly | Pro | His | Pro | His | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Ile | Lys | Leu | Glu | Asn | Pro | Leu | Asp | Tyr | Gly | Ser | Ala | Trp | Ala | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Ala | Ala | Gln | Cys | Arg | Tyr | Gly | Asp | Leu | Ala | Ser | Leu | His | Gly | Ala |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Ala | Ala | Gly | Pro | Gly | Ser | Gly | Ser | Pro | Ser | Ala | Ala | Ala | Ser | Ser |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Trp | His | Thr | Leu | Phe | Thr | Ala | Glu | Glu | Gly | Gln | Leu | Tyr | Gly | Pro |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Cys | Gly | Ala | Gly |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Ala | Gly | Ala | Val | Ala | Pro | Tyr | Gly | Tyr | Thr | Arg | Pro | Pro | Gln | Gly |

|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |              |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------------|-----|-----|-----|
| Leu | Ala | Gly | Gln | Glu | Gly | Asp | Phe | Thr | Ala | Pro | Asp | Val          | Trp | Tyr | Pro |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |              |     |     | 480 |
| Gly | Gly | Met | Val | Ser | Arg | Val | Pro | Tyr | Pro | Ser | Pro | Thr          | Суз | Val | Lys |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |              |     | 495 |     |
| Ser | Glu | Met | Gly | Pro | Trp | Met | Asp | Ser | Tyr | Ser | Gly | Pro          | Tyr | Gly | Asp |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |              | 510 |     |     |
| Met | Arg | Leu | Glu | Thr | Ala | Arg | Asp | His | Val | Leu | Pro | Ile          | Asp | Tyr | Tyr |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525          |     |     |     |
| Phe | Pro | Pro | Gln | Lys | Thr | Cys | Leu | Ile | Cys | Gly | Asp | Glu          | Ala | Ser | Gly |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |              |     |     |     |
| Cys | His | Tyr | Gly | Ala | Leu | Thr | Cys | Gly | Ser | Суз | Lys | Val          | Phe | Phe | Lys |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |              |     |     | 560 |
| Arg | Ala | Ala | Glu | Gly | Lys | Gln | Lys | Tyr | Leu | Суз | Ala | Ser          | Arg | Asn | Asp |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |              |     | 575 |     |
| Cys | Thr | Ile | Asp | Lys | Phe | Arg | Arg | Lys | Asn | Cys | Pro | Ser          | Cys | Arg | Leu |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |              | 590 |     |     |
| Arg | Lys | Cys | Tyr | Glu | Ala | Gly | Met | Thr | Leu | Gly | Ala | Arg          | Lys | Leu | Lys |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605          |     |     |     |
| Lys | Leu | Gly | Asn | Leu | Lys |     | Gln | Glu | Glu | Gly | Glu | Ala          | Ser | Ser | Thr |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |              |     |     |     |
| Thr | Ser | Pro | Thr | Glu | Glu | Thr | Ala | Gln | Lys | Leu | Thr | Val          | Ser | His |     |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |              |     |     | 640 |
| Glu | Gly | Tyr | Glu | -   | Gln | Pro | Ile | Phe |     | Asn | Val | Leu          | Glu |     | Ile |
|     |     |     |     | 645 |     | _   |     |     | 650 |     |     |              |     | 655 |     |
| Glu | Pro | Gly |     | Val | Суѕ | Ala | Gly |     | Asp | Asn | Asn | Gln          | Pro | Asp | Ser |
|     |     | _   | 660 |     | _   | _   | _   | 665 |     |     |     |              | 670 |     | _   |
| Phe | Ala |     | Leu | Leu | Ser | Ser |     | Asn | Glu | Leu | Gly |              | Arg | GIn | Leu |
| _   |     | 675 |     |     |     | _ • | 680 |     |     |     |     | 685          | _   | _   | _   |
| Val |     | Val | Val | Lys | Trp |     | Lys | Ala | Leu | Pro |     | Phe          | Arg | Asn | Leu |
|     | 690 |     |     |     |     | 695 | _   | _   | _   |     | 700 |              |     |     |     |
|     | Val | Asp | Asp | Gln |     | Ala | Val | Ile | Gln | -   | Ser | Trp          | Met | Gly |     |
| 705 |     | _   | _   |     | 710 | _   |     |     | _   | 715 |     | <del>-</del> | _   | _   | 720 |
| Met | Val | Phe | Ala |     | Gly | Trp | Arg | Ser |     | Thr | Asn | Val          | Asn |     | Arg |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |              |     | 735 |     |

| Met | Leu | Tyr | Phe | Ala | Pro | Asp | Leu | Val | Phe | Asn | Glu | Tyr | Arg | Met | His |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Lys | Ser | Arg | Met | Tyr | Ser | Gln | Cys | Val | Arg | Met | Arg | His | Leu | Ser | Gln |
|     |     | 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Glu | Phe | Gly | Trp | Leu | Gln | Ile | Thr | Pro | Gln | Glu | Phe | Leu | Cys | Met | Lys |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
| Ala | Leu | Leu | Leu | Phe | Ser | Ile | Ile | Pro | Val | Asp | Gly | Leu | Lys | Asn | Gln |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |
| Lys | Phe | Phe | Asp | Glu | Leu | Arg | Met | Asn | Tyr | Ile | Lys | Glu | Leu | Asp | Arg |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |
| Ile | Ile | Ala | Cys | Lys | Arg | Lys | Asn | Pro | Thr | Ser | Cys | Ser | Arg | Arg | Phe |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |
| Tyr | Gln | Leu | Thr | Lys | Leu | Leu | Asp | Ser | Val | Gln | Pro | Ile | Ala | Arg | Glu |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |
| Leu | His | Gln | Phe | Thr | Phe | Asp | Leu | Leu | Ile | Lys | Ser | His | Met | Val | Ser |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |
| Val | Asp | Phe | Pro | Glu | Met | Met | Ala | Glu | Ile | Ile | Ser | Val | Gln | Val | Pro |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |
| Lys | Ile | Leu | Ser | Gly | Lys | Val | Lys | Pro | Ile | Tyr | Phe | His | Thr | Gln |     |
|     |     |     |     | 885 |     |     |     |     | 890 |     |     |     |     | 895 |     |
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| gaggagcttt | ccagaatctg | ttccagagcg | tgcgcgaagt | gatccagaac | ccgggcccca | 540  |
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| tgagtccagg | ggaacagctt | cggggggatt | gcatgtacgc | cccagttttg | ggagttccac | 1200 |
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<400> 4

130

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135

140

| Ser | Thr | Leu | Ser | Leu | Leu | Gly | Pro | Thr | Phe | Pro | Gly | Leu | Ser | Ser | CAa |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ala | Asp | Leu | Lys | Asp | Ile | Leu | Ser | Glu | Ala | Ser | Thr | Met | Gln | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Gln | Gln | Gln | Gln | Gln | Glu | Ala | Val | Ser | Glu | Gly | Ser | Ser | Ser | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ala | Arg | Glu | Ala | Ser | Gly | Ala | Pro | Thr | Ser | Ser | Lys | Asp | Asn | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gly | Gly | Thr | Ser | Thr | Ile | Ser | Asp | Ser | Ala | Lys | Glu | Leu | Cys | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Val | Ser | Val | Ser | Met | Gly | Leu | Gly | Val | Glu | Ala | Leu | Glu | His | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Pro | Gly | Glu | Gln | Leu | Arg | Gly | Asp | Cys | Met | Tyr | Ala | Pro | Val | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Val | Pro | Pro | Ala | Val | Arg | Pro | Thr | Pro | Суз | Ala | Pro | Leu | Ala | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Cys | Lys | Gly | Ser | Leu | Leu | Asp | Asp | Ser | Ala | Gly | Lys | Ser | Thr | Glu | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Ala | Glu | Tyr | Ser | Pro | Phe | Lys | Gly | Gly | Tyr | Thr | Lys | Gly | Leu | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Glu | Ser | Leu | Gly | Cys | Ser | Gly | Ser | Ala | Ala | Ala | Gly | Ser | Ser | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Leu | Glu | Leu | Pro | Ser | Thr | Leu | Ser | Leu | Tyr | Lys | Ser | Gly | Ala | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Glu | Ala | Ala | Ala | Tyr | Gln | Ser | Arg | Asp | Tyr | Tyr | Asn | Phe | Pro | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Leu | Ala | Gly | Pro | His | Pro | His | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Ile | Lys | Leu | Glu | Asn | Pro | Leu | Asp | Tyr | Gly | Ser | Ala | Trp | Ala | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Ala | Ala | Gln | Cys | Arg | Tyr | Gly | Asp | Leu | Ala | Ser | Leu | His | Gly | Ala |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Ala | Ala | Gly | Pro | Gly | Ser | Gly | Ser | Pro | Ser | Ala | Ala | Ala | Ser | Ser |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Trp | His | Thr | Leu | Phe | Thr | Ala | Glu | Glu | Gly | Gln | Leu | Tyr | Gly | Pro |

|           |            |         | 420        |          |       |          |              | 425        |     |       |       |          | 430      |      |          |
|-----------|------------|---------|------------|----------|-------|----------|--------------|------------|-----|-------|-------|----------|----------|------|----------|
| Cys       | Gly        | Gly     | Gly        | Gly      | Gly   | Gly      | Gly          | Gly        | Gly | Gly   | Gly   | Gly      | Gly      | Ala  | Gly      |
|           |            | 435     |            |          |       |          | 440          |            |     |       |       | 445      |          |      |          |
| Glu       | Ala        | Gly     | Ala        | Val      | Ala   | Pro      | Tyr          | Gly        | Tyr | Thr   | Arg   | Pro      | Pro      | Gln  | Gly      |
|           | 450        |         |            |          |       | 455      |              |            |     |       | 460   |          |          |      |          |
| Leu       | Ala        | Gly     | Gln        | Glu      | Gly   | Asp      | Phe          | Thr        | Ala | Pro   | Asp   | Val      | Trp      | Tyr  | Pro      |
| 465       |            |         |            |          | 470   |          |              |            |     | 475   |       |          |          |      | 480      |
| Gly       | Gly        | Met     | Val        | Ser      | Arg   | Val      | Pro          | Tyr        | Pro | Ser   | Pro   | Thr      | Cys      | Val  | Lys      |
|           |            |         |            | 485      |       |          |              |            | 490 |       |       |          |          | 495  |          |
| Ser       | Glu        | Met     | Gly        | Pro      | Trp   | Met      | Asp          | Ser        | Tyr | Ser   | Gly   | Pro      | Tyr      | Gly  | Asp      |
|           |            |         | 500        |          |       |          |              | 505        |     |       |       |          | 510      |      |          |
| Met       | Arg        | Leu     | Glu        | Thr      | Ala   | Arg      | Asp          | His        | Val | Leu   | Pro   | Ile      | Asp      | Tyr  | Tyr      |
|           |            | 515     |            |          |       |          | 520          |            |     |       |       | 525      |          |      |          |
| Phe       | Pro        | Pro     | Gln        | Lys      | Thr   | Cys      | Leu          | Ile        | Сув | Gly   | Asp   | Glu      | Ala      | Ser  | Gly      |
|           | 530        |         |            |          |       | 535      |              |            |     |       | 540   |          |          |      |          |
| Суѕ       | His        | Tyr     | Gly        | Ala      | Leu   | Thr      | Суѕ          | Gly        | Ser | Cys   | Lys   | Val      | Phe      | Phe  | Lys      |
| 545       |            |         |            |          | 550   |          |              |            |     | 555   |       |          |          |      | 560      |
| Arg       | Ala        | Ala     | Glu        | Gly      | Lys   | Gln      | Lys          | Tyr        | Leu | Cys   | Ala   | Ser      | Arg      |      | Asp      |
|           |            |         |            | 565      |       |          |              |            | 570 |       |       |          |          | 575  |          |
| Cys       | Thr        | Ile     | Asp        | Lys      | Phe   | Arg      | Arg          |            | Asn | Cys   | Pro   | Ser      | Cys      | Arg  | Leu      |
|           |            |         | 580        |          |       |          |              | 585        |     |       |       |          | 590      |      |          |
| Arg       | Lys        | _       | Tyr        | Glu      | Ala   | Gly      |              | Thr        | Leu | Gly   | Ala   |          | Lys      | Leu  | Lys      |
|           |            | 595     |            |          |       |          | 600          |            |     |       |       | 605      | _        | _    |          |
| Lys       |            | Gly     | Asn        | Leu      | Lys   |          | Gln          | GLu        | Glu | СТĀ   |       | Ala      | Ser      | Ser  | Thr      |
| _,        | 610        | _       | _,         |          | ~1    | 615      |              | <b>~</b> 1 |     | _     | 620   | 1        | <b>~</b> | •••  |          |
|           | Ser        | Pro     | Thr        | GIu      |       | Thr      | Ala          | GIn        | ьуs |       | Thr   | Val      | Ser      | His  |          |
| 625       | <b>0</b> 3 | <b></b> | <b>03</b>  | <b>a</b> | 630   | <b>5</b> | -7.          | Dla a      | T   | 635   | ** 1  | <b>.</b> | a1       | 21-  | 640      |
| GIU       | GIĀ        | туг     | Glu        |          | GIU   | Pro      | TTE          | Pile       |     | ASII  | vai   | ьeu      | GIU      |      | тте      |
| <b>~1</b> | Dwo        | C111    | 770 J      | 645      | C     | 71-      | ~1. <i>r</i> | uic        | 650 | y az  | 7 an  | C1~      | Dro      | 655  | Cor      |
| GIU       | PIO        | СТА     | Val<br>660 | Val      | Cys   | ALG      | GTĀ          | 665        | Map | ASII  | ASII  | GIII     | 670      | ASD  | Ser      |
| Dha       | Δla        | λla     | Leu        | Lou      | gor.  | Sor      | T.011        |            | Glu | T.011 | Glv   | Glu      |          | Gln  | T.OII    |
| 1116      | 1114       | 675     | ±cu        | пец      | ner   | Der      | 680          | 11,511     |     | Leu   | O.L.Y | 685      | **** 9   | 0411 | <u> </u> |
| Val       | His        |         | Val        | Lve      | ינינו | Ala      |              | Ala        | Len | Pro   | Glv   |          | Ara      | Asn  | Lev      |
|           | 690        |         |            | -1.0     | 12    | 695      |              |            |     | •     | 700   |          | 3        |      |          |

| His | Val | Asp | Asp | Gln | Met | Ala | Val | Ile | Gln | Tyr | Ser | Trp | Met | Gly | Leu |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Met | Val | Phe | Ala | Met | Gly | Trp | Arg | Ser | Phe | Thr | Asn | Val | Asn | Ser | Arg |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |
| Met | Leu | Tyr | Phe | Ala | Pro | Asp | Leu | Val | Phe | Asn | Glu | Tyr | Arg | Met | His |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Lys | Ser | Arg | Met | Tyr | Ser | Gln | Cys | Val | Arg | Met | Arg | His | Leu | Ser | Gln |
|     |     | 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Glu | Phe | Gly | Trp | Leu | Gln | Ile | Thr | Pro | Gln | Glu | Phe | Leu | Cys | Met | Lys |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
| Ala | Leu | Leu | Leu | Phe | Ser | Ile | Ile | Pro | Val | Asp | Gly | Leu | Lys | Asn | Gln |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |
| Lys | Phe | Phe | qaA | Glu | Leu | Arg | Met | Asn | Tyr | Ile | Lys | Glu | Leu | Asp | Arg |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |
| Ile | Ile | Ala | Cys | Lys | Arg | Lys | Asn | Pro | Thr | Ser | Cys | Ser | Arg | Arg | Phe |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |
| Tyr | Gln | Leu | Thr | Lys | Leu | Leu | Asp | Ser | Val | Gln | Pro | Ile | Ala | Arg | Glu |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |
| Leu | His | Gln | Phe | Thr | Phe | Asp | Leu | Leu | Ile | Lys | Ser | His | Met | Val | Ser |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |
| Val | Asp | Phe | Pro | Glu | Met | Met | Ala | Glu | Ile | Ile | Ser | Val | Gln | Val | Pro |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |
| Lys | Ile | Leu | Ser | Gly | Lys | Val | Lys | Pro | Ile | Tyr | Phe | His | Thr | Gln |     |
|     |     |     |     | 885 |     |     |     |     | 890 |     |     |     |     | 895 |     |
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<211> 3175

<212> DNA

<213> Macaca mulatta

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taagaacaaa aaagaaaatt ctagcccgta gaaaacttag atggggagtt cacaattctc 180
tgtctgacac tcggatcgtc ccgtctagaa caggtggcac acagaagaaa acgtcctctg 240

| aaactccgac | agtctcgcga | aaaacgcacc | aacgagggcg | ttcaaaggaa | gagacctcga | 300  |
|------------|------------|------------|------------|------------|------------|------|
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|            | cttcccctcc |            |            |            |            | 420  |
|            | cgtcaatccc |            |            |            |            | 480  |
|            | ggtcttagac |            |            |            |            | 540  |
|            | ccggcgctcg |            |            |            |            | 600  |
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|            | agcatctccg |            |            |            |            | 720  |
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| ggcggcaccg | gcggccgttc | cccgacggcg | tcgtcgacgg | tcgtggaggc | ctgctcctac | 840  |
| tgagtcgacg | gggtaggtgc | aacagagacg | acccggggtg | aaaggggccg | aattcgtcga | 900  |
| cgaggcggct | ggaatttctg | taggactcgc | tccggtcgtg | gtacgttgag | gaagtcgttg | 960  |
| tcgtcgtcct | tcgtcatagg | cttccgtcgt | cgtcgccctc | tcgctccctc | cggagccccc | 1020 |
| gagggtgaag | gaggttcctg | ttaatgaatc | tcccgtgaag | ctggtaaaga | ctgtcgcggt | 1080 |
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| cctgtgaact | tgacggcagg | tgggacagag | agatgttcag | gcctcgtgac | ctgctccgtc | 1440 |
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| gaggtggcgg | aggggtaggg | gtgcgagcgt | agttcgacct | cttgggcgac | ctgataccgt | 1560 |
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| gagagaagtg | tcggcttctt | ccggtcaaca | tacctggcac | accaccaccc | ccgccgccgc | 1740 |
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| ccggtggagt | ccccgaccgc | ccggtccttc | cgctgaagtg | gcgtggacta | cacaccatgg | 1860 |
| gaccgccgta | ccactcgtct | cacgggatag | ggtcagggtg | aacacagttt | tcgctctacc | 1920 |
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| tacttcgaag | acccacagtg | atacctcgag | agtgtacacc | ttcgacgttc | cagaagaagt | 2100 |
| tttctcggcg | acttcccttt | gtcttcatgg | acacacggtc | gtctttacta | acgtgataac | 2160 |
| tatttaaggc | ttccttttta | acaggtagaa | cggcagaagc | ctttacaata | cttcgtccct | 2220 |
| actgagaccc | tcgggccttc | gacttctttg | aaccattaga | ctttgatgtc | ctccttcctc | 2280 |
| tccgaaggtc | gtggtggtcg | gggtgactcc | tctgtcgggt | cttcgactgt | cacagtgtgt | 2340 |

| aacttccgat | acttacagtc | gggtagaaag | acttacagga | cctccggtaa | ctcggtccac | 2400 |
|------------|------------|------------|------------|------------|------------|------|
| accacacacg | acctgtactg | ttgttggtcg | ggctgaggaa | gcgtcggaac | gagagatcgg | 2460 |
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| cgaaggcgtt | gaatgtgcac | ctgctggtct | accgacagta | agtcatgagg | acctaccccg | 2580 |
| agtaccacaa | acggtacccg | accgctagga | agtggttaca | gttgaggtcc | tacgagatga | 2640 |
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| cacaggctta | ctccgtggag | agagttctca | aacctaccga | ggtttagtgg | ggggtcctta | 2760 |
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| gtgtgtacca | ctcgcacctg | aaaggccttt | actaccgtct | ctagtagaga | cacgttcacg | 3060 |
| ggttctagga | aagacccttt | cagttcgggt | agataaaggt | gtgggtcact | tcgtaacctt | 3120 |
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<211> 2821

<212> DNA

<213> Macaca fascicularis

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| 120 | gggccccagg | tccagaaccc | cgċgaagtga | ccagagcgtg | agaatctgtt | ggagctttcc |
| 180 | gcagcagcag | tgcagcagca | ggcgccagtt | agcacctccc | ccgcgagcgc | cacccagagg |
| 240 | tggttctccc | agggtgagga | cagcagcagc | gcaacagcag | ctagcccccg | cagcaagaaa |
| 300 | gcagccttca | atgaggaaca | ctggtcctgg | cacaggctac | gtagaggccc | caagcccatc |
| 360 | gcctggagcc | gcgtcccaga | gagagaggtt | gtgccacccc | cagccccgga | cagcctcagt |
| 420 | cgaggatgac | cacctccgga | cagctgccag | gctgccgcag | ccggcaaggg | gccgtggccg |
| 480 | aagcagctgc | tccccggctt | ggccccactt | gtctctgctg | catccacgtt | tcagctgccc |
| 540 | tcagcaacag | tgcaactcct | gccagcacca | cctgagcgag | ttaaagacat | tccaccgacc |
| 600 | ctcgggggct | ccagggaggc | agcgggagag | aggcagcagc | cagtatccga | cagcaggaag |
| 660 | cagcgccaag | ccatttctga | ggcacttcga | ttacttaggg | ccaaggacaa | cccacttcct |
| 720 | ggagcatctg | tggaggcgtt | ggcttgggtg | ggtgtccatg | aggcagtgtc | gagctgtgta |
| 780 | agttccaccc | cagttttggg | atgtacgccc | gggggattgc | aacagcttcg | agtccagggg |
| 840 | gctagacgac | aaggttctct | gccgaatgca | tgccccattg | ccactccgtg | gctgtgcgtc |

| agcgcaggca | agagcactga | agatactgct | gagtattccc | ctttcaaggg | aggttacacc | 900  |
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| acacttgaac | tgccgtccac | cctgtctctc | tacaagtccg | gagcactgga | cgaggcagct | 1020 |
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| ggcggcggcg | gcggcggcgc | aggcgaggcg | ggagctgtag | cccctacgg  | ctacactcgg | 1380 |
| ccacctcagg | ggctggcggg | ccaggaaggc | gacttcaccg | cacctgatgt | gtggtaccct | 1440 |
| ggcggcatgg | tgagcagagt | gccctatccc | agtcccactt | gtgtcaaaag | cgagatgggc | 1500 |
| ccctggatgg | atagctactc | cggaccttac | ggggacatgc | ggttggagac | tgccagggac | 1560 |
| catgttttgc | caattgacta | ttactttcca | ccccagaaga | cctgcctgat | ctgtggagat | 1620 |
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| gcttccagca | ccaccagccc | cactgaggag | acagcccaga | agctgacagt | gtcacacatt | 1920 |
| gaaggctatg | aatgtcagcc | catctttctg | aatgtcctgg | aagccattga | gccaggtgtg | 1980 |
| gtgtgtgctg | gacatgacaa | caaccagccc | gactccttcg | cagccttgct | ctctagcctc | 2040 |
| aatgaactgg | gagagagaca | gcttgtacat | gtggtcaagt | gggccaaggc | cttgcctggc | 2100 |
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| ccctatttcc | tcaccccagc | tcatgccccc | tttcagatgt | cttctgcctg | ttataactct | 2760 |
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| <212> DNA   |     |
| <213> Macaca mulatta  |     |
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| cgaatgaact acatcaagga actcgatcgt atcattgcat gcaaaagaaa aaatcccaca | 180 |
| tcctgctcaa ggcgtttcta ccagctcacc aagctcctgg actccgtgca gcctattgcg | 240 |
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|   |     |
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|        |                     |    |
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| <223>  | PCR primer          |    |
|        |                     |    |
| <400>  |                     | ۰. |
| ggcggc | egag ggtagaccet c   | 21 |

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## INTERNATIONAL SEARCH REPORT

International application No.

|  | PCT/US02/14175  |  |  |  |  |
|--|---|--|--|--|--|
| A. CLASSIFICATION OF SUBJECT MATTER  |   |  |  |  |  |
| IPC(7) : C12N 5/10, 15/09, 15/11, 15/12, 15/63   | •   |  |  |  |  |
| US CL : 435/69.1, 320.2, 325; 536/23.5   |   |  |  |  |  |
| According to International Patent Classification (IPC) or to both  | national classification and IPC   |  |  |  |  |
| B. FIELDS SEARCHED   |   |  |  |  |  |
| Minimum documentation searched (classification system followed   | hv classification symbols)  |  |  |  |  |
| U.S.: 435/69.1, 320.2, 325; 536/23.5   | of valuation of the conf  |  |  |  |  |
| Older 1 - tool or (2) one (2) one ; cool or or   |   |  |  |  |  |
|  |   |  |  |  |  |
| Documentation searched other than minimum documentation to the   | ne extent that such documents are included in the fields searched   |  |  |  |  |
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| Please See Continuation Sheet  |   |  |  |  |  |
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| C. DOCUMENTS CONSIDERED TO BE RELEVANT   |   |  |  |  |  |
| Category * Citation of document, with indication, where a  | ppropriate, of the relevant passages Relevant to claim No.  |  |  |  |  |
| A CHOONG et al. Evolution of the primate androger  |   |  |  |  |  |
| disease. 1998, Vol. 47, No. 3, pages 334-342, see  |   |  |  |  |  |
| (130036. 1370, 101. 77, 110. 5, pages 554 574, 500   | entine reference.   |  |  |  |  |
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| Further documents are listed in the continuation of Box C.   |   |  |  |  |  |
|  | See patent family annex.  |  |  |  |  |
| Special categories of cited documents:   | "I" later document published after the international filing date or priority  |  |  |  |  |
| "A" document defining the general state of the art which is not considered to be   | date and not in conflict with the application but cited to understand the<br>principle or theory underlying the invention                   |  |  |  |  |
| of particular relevance  |   |  |  |  |  |
| "E" earlier application or patent published on or after the international filing date  | "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step |  |  |  |  |
|  | when the document is taken alone  |  |  |  |  |
| "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as | "Y" document of particular relevance; the claimed invention cannot be   |  |  |  |  |
| specified)   | considered to involve an inventive step when the document is  |  |  |  |  |
| "O" document referring to an oral disclosure, use, exhibition or other means   | combined with one or more other such documents, such combination  |  |  |  |  |
| document reterring to an oral discressive, use, evinously of other means   | being obvious to a person skilled in the art  |  |  |  |  |
| "P" document published prior to the international filing date but later than the   | "&" document member of the same patent family   |  |  |  |  |
| priority date claimed  |   |  |  |  |  |
| Date of the actual completion of the international search  | Date of mailing of the international search report  23 SEP 2002  Authorized officer  Calence Boll-Harro for Michael Pak                     |  |  |  |  |
| 23 SFP 2002  |   |  |  |  |  |
| 26 July 2002 (26.07.2002)  | 400E. LUUL  |  |  |  |  |
| Name and mailing address of the ISA/US  Commissioner of Patents and Trademarks   | Authorized officer 12 all - Hanne and   |  |  |  |  |
| Commissioner of Patents and Trademarks  Box PCT  | Michael Pak   |  |  |  |  |
| Washington, D.C. 20231   | _   |  |  |  |  |
| Facsimile No. (703)305-3230  | Telephone No. 703-308-1235  |  |  |  |  |

# SEST AVAILABLE COPY

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/14175

| Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)                           |   |
|---|---|
| This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons: |   |
| 1.  | Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:  |
| 2.  | Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically: |
| 3<br>6.4(a)   | Claim Nos.:  because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule .  |
| Вох П О   | bservations where unity of invention is lacking (Continuation of Item 2 of first sheet)   |
|   | ational Searching Authority found multiple inventions in this international application, as follows:<br>Continuation Sheet  |
| 1.  | As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.  |
| 2.  | As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.  |
| 3.  | As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:                      |
| 4. 🔀  | No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-24     |
| Remark on   | Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.   |
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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/14175

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-24, drawn to a purified DNA molecule, DNA expression vector, host cell, and a process for expressing the protein.

Group II, claim(s) 25-28, drawn to a purified Macaca mulatta AR protein.

Group III, claim(s) 29-54, drawn to a purified DNA molecule, DNA expression vector, host cell, and a process for expressing the protein.

Group IV, claim(s) 55-58, drawn to a purified Macaca mulatta AR protein.

The inventions listed as Groups I-IV do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The special technical feature of Group I is a DNA molecule, DNA expression vector, host cell, and a process for expressing the protein. Pursuant to 37 CFR 1.475(d), these claims are considered by the ISA/US to constitute the main invention, and none of the related groups II-XII correspond to the main invention.

The products of Group II-IV do not share the same or corresponding special technical feature with Group I, because they are drawn to products having materially different structures and functions, and each defines a separate invention over the art.

Since Groups I-IV do not share a special technical feature, unity of invention is lacking.

Continuation of B. FIELDS SEARCHED Item 3: BRS, GENEMBL, MEDLINE, NGENESEQ, EST

search terms: androgen receptor, Macaca Mulatta, nuclear receptor, steroid receptor